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(54) Title: DIABETES–MEDIATING PROTEINS AND THERAPEUTIC USES THEREOF

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                MISASRAAAARLVGTAASRSPAAARPQDGWNGLSHEAFRFVSR
DYASEAIKGAVVGIDLGTTNSCVAVMEGKQAKVLENAEGARTTPSVVAFTADGERLV
MPAKRQAVTNPNNTFYATKRLIGRRYDDPEVQKDTKNVPFKIVRASNGDAWVEAHGK
YSPSQIGAFVLMKMKETAENYLGHTAKNAVITVPAYFNDSQRQATKDAGQISGLNVL
VINEPTAAALAYGLDKSEDKVIAVYDLGGGTFDISILEIQKGVFEVKSTNGDTFLGG
DFDQALLRHIVKEFKRETGVDLTKDNMALQRVREAAEKAKCELSSSVQTDINLPYLT
DASGPKHLNMKLTRAQFEGIVTDLIKRTIAPCQKAMQDAEVSKSDIGEVILVGGMTR
PKVQQTVQDLFGRAPSKAVNPDEAVAIGAAIQGGVLAGDVTDVLLLDVTPLSLGIET
GGVFTKLINRNTTIPTKKSQVFSTAADGQTQVEIKVCQGEREMAGDNKLLGQFTLIG
PPAPRGVPQIEVTFDIDANGIVHVSAKDKGTGREQQIVIQSSGGLSKDDIENMVKNA
KYAEEDRRKKERVEAVNMAEGIIHDTETKMEEFKDQLPADECNKLKEBISKVRALLA
KDSETGENIRQAASSLQQASLKLFEMAYKKMASEREGSGSSGTGEQKEDQKEEKQ
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(57) Abstract

Provided are protective and deleterious diabetes–mediating proteins and polynucleotides encoding same, transgenic animals expressing a diabetes–mediating protein, drug screening methods for identifying a test compound capable of altering the expression of a diabetes–mediating protein, and methods of preventing or ameliorating diabetes by administering a compound capable of altering the expression of a diabetes–mediating protein.

DIABETES-MEDIATING PROTEINS AND THERAPEUTIC
USES THEREOF

Background of the Invention

Field of the Invention

5   This invention relates generally to diabetes-mediating proteins, methods of identifying diabetes-mediating proteins, transgenic animals useful in the assays of the invention, methods for screening for drugs which affect the expression of diabetes-mediating proteins, and therapeutic compounds for the treatment and prevention of diabetes.

10   ### Related Art

The development of insulin-dependent diabetes mellitus (IDDM) in man, and in animal models of human disease, is characterized by mononuclear cell infiltration and, β-cell destruction in the pancreatic islets (insulitis). The mechanisms behind β-cell destruction is not known. Accumulating evidence indicates that the cytokine interleukin-1,6
15   (IL-1β), primarily produced by macrophages and monocytes, may be a mediator of islet, β-cell destruction.

Animal models of human diabetes include diabetes-prone BB (BB-DP) rats and non-obese diabetic (NOD) mice. 2-Dimensional (2D) gel maps of rat islet proteins have been constructed and used to determine qualitative and quantitative changes in protein
20   synthesis resulting with *in vitro* exposure of rat islet cells to IL-1β (Andersen *et al.* *Diabetes* 44:400-407 (1995)).

Transgenic animal models of human diseases are known. For example, one model for human diabetes is a transgenic mouse expressing a viral protein in the pancreatic β cells under control of the rat insulin promoter (van Herrath *et al.* *J. Clin. Invest.* 98:1324-1331
25   (1996)). Less than 2% of the transgenic mice develop diabetes spontaneously; however, after a 2 month challenge with the virus, IDDM occurs in more than 95% of the mice.

Summary of the Invention

The invention is based, in part, on the discovery and identification of diabetes-mediating (DM) proteins. DM proteins are proteins which are involved in the development
30   of diabetes or in the prevention of diabetes development in a subject at risk for the development of diabetes, and are identified by differential expression during the presence

and absence of disease development. The development of diabetes includes all stages which precede the clinically detectable stage.

Accordingly, in one aspect the invention features substantially purified diabetes-mediating proteins exhibiting an altered expression during development of diabetes relative to expression in the absence of diabetes development. The purified diabetes-mediating proteins of the invention are selected from the proteins listed in Tables 1 and 2. Novel diabetes-mediating proteins are provided characterized by molecular weight, pI, and the mass spectroscopic characteristics as shown in FIGs. 6-40. These proteins, referred to by their position on 10% IEF or NEPHGE 2-dimensional gels (FIGs. 1A-1B), are selected from the group consisting of NEPHGE 7, 9, 102, 123, 129,130, 174, 181, 182, 211, 231, 236, 253, 298, and IEF 665, 939, 941, 950, 1196.

DM proteins are further characterized as protective or deleterious DM proteins. A protective diabetes-mediating protein ("protective protein") is characterized as a protein capable of protecting against the development of diabetes and/or delaying the onset of diabetes in a subject at risk for development of diabetes, or ameliorating the symptoms of diabetes in a subject suffering from diabetes. A protective protein may also be a protein which does not alter expression during development of diabetes, but exhibits an altered expression in a subject at risk for diabetes who escapes the development of diabetes. A deleterious diabetes-mediating protein ("deleterious protein") is characterized as a protein capable of enhancing the development of diabetes, increasing the risk of a subject developing diabetes, or reducing the time required for development of diabetes in a subject at risk for development of diabetes. A deleterious protein may also be a protein which does not alter expression during development of diabetes, but exhibits an altered expression in a subject at risk for diabetes who escapes the development of diabetes. The diabetes-mediating protein of the invention may be identified by any means known to the art, including gel electrophoresis, immunoblotting, mass spectrometry, or chromatography, and is characterized by an altered protein expression during development of diabetes as compared to the same protein expressed in the absence of diabetes development. U.S. provisional patent application Serial No. 60/029,324 identifies proteins expressed in pancreatic islet cells identified by molecular weight and pI (FIGs. 1A and 1B). The instant application provides a selection of these proteins which have been identified as diabetes-mediating proteins, as listed in Tables 1 and 2, and FIGs. 6-40.

The diabetes-mediating proteins of the invention are useful in drug screening assays for identifying compounds capable of modulating the development of diabetes, useful as therapeutic agents for the treatment or prevention of diabetes, and useful as targets of therapeutic agents capable of preventing or ameliorating diabetes by modulating the expression of the diabetesmediating protein.

Changes in the expression of specific DM proteins is diagnostically useful as indicative of the development of diabetes. Accordingly, in one aspect the invention

features a method for diagnosing the development of diabetes by measuring an increase in protein expression in one or more proteins selected from the group consisting of the diabetes-mediating proteins listed in Table 1, and a decrease in the protein expression of one or more proteins selected from the list consisting of the diabetes-mediating proteins listed in Table 2. Changes in protein expression are measured in a test subject suspected of developing diabetes or at risk for the development of diabetes and are expressed relative to protein expression in a normal non-diabetes control. In a preferred embodiment, changes of combinations of one or more of the proteins of Tables 1 and 2 is indicative of the development of diabetes. In a more preferred embodiment, changes of a combination of 5 or more of the proteins of Tables 1 and/or 2 is indicative of the development of diabetes. In an even more preferred embodiment, changes of a combination of 10 or more of the proteins of Tables 1 and/or 2 is indicative of the development of diabetes.

In one aspect, the invention features an *in vivo* assay method for identifying proteins which are involved in the development of disease, e.g., diabetes. In a specific embodiment of the *in vivo* assay method of the invention, cells which secret insulin or are capable of developing into insulinproducing cells are transplanted to an immunologically compatible host animal which is an animal at risk for the development of diabetes. Protein expression is analyzed in transplanted cells rescued at time points between the time of transplantation and disease onset, and proteins exhibiting an altered expression during disease development relative to their expression in the absence of the development of diabetes are identified. In specific embodiments, the transplanted cells are neonatal islet cells which are transplanted into a animal model at risk for development of diabetes. In one specific embodiment, the neonatal islet cells are taken from neonatal BB-DP rats and the host animal is BB-DP rat. In another embodiment, the source of transplanted cells and host animals are NOD mice.

The invention provides identified diabetes-mediating proteins which may be further characterized as protective or deleterious proteins. In one embodiment of the invention, a candidate protective or deleterious protein is identified *in vitro* by transfecting cultured cells with a polynucleotide encoding the candidate protective or deleterious protein, and the effect of expression of the diabetes-mediating protein on *in vitro* cell functionality upon challenge with IL-1β determined. The polynucleotide may be operably connected to an inducible promoter such that expression of the candidate protective or deleterious protein is under exogenous control. Exogenous control may be exerted by agents, e.g., interferon, such agents being determined by the promoter selected. In specific embodiments, cell functionality is determined by measurement of nitric oxide (NO) production, insulin secretion, cell survival, and/or cytotoxicity upon exposure to IL-1β.

In an *in vivo* method for identifying protective or deleterious diabetes-mediating proteins, a transgenic mammal is generated expressing the candidate protein, wherein the transgenic mammal is at risk for developing diabetes, and the effect of transgene

expression on the development and timing of diabetes onset is determined. A protective protein is one which prevents, inhibits, or slows the development of diabetes in a subject at risk for diabetes, and a deleterious protein is one that causes the development of diabetes, increases the risk of development of diabetes, or decreases the time required for
5   the development of diabetes in a subject at risk for developing diabetes. A deleterious protein is also a protein that prevents or interferes with the expression of a protective protein.

        The invention includes a substantially purified protective or deleterious diabetes-mediating protein, and polynucleotide sequence which encodes the diabetes-mediating
10   protein of the invention. In one non-limiting embodiment, the protective protein is galactin-3 (FIGs. 4 and 5) (SEQ ID NOs:1-2). In another non-limiting embodiment, the deleterious protein is mortalin (FIGs. 2-3) (SEQ ID NOs:3-4).

        In one aspect, the invention features a transgenic mammal having an exogenous diabetesmediating protein gene or genes inserted into its genome. The transgenic mammal
15   of the invention is useful in assay methods for determining the effect of the expression of a diabetes-mediating protein in the development of diabetes, and for identifying protective or deleterious proteins. The transgene may be a natural, or partially or wholly artificial diabetes-mediating gene, and may be different from or the same as an endogenous diabetes-mediating protein gene. In one embodiment, the transgene is under control of an
20   inducible promoter.

        In a related aspect, the invention features a transgenic mammal having an exogenous deleterious gene, and exhibiting an increased incidence of the spontaneous development of diabetes within a predictable period of time. In preferred embodiments, the transgenic mammal exhibits a greater than 50% chance, more preferably a greater than
25   60% chance, even more preferably a greater than 70% chance, even more preferably a greater than 80% chance, and most preferably a greater than 90% chance of developing diabetes. In an embodiment of the invention, the transgenic mammal of the invention is transgenic for one or more genes encoding a deleterious diabetes-mediating protein. In another embodiment, the transgenic mammal additionally has one or more endogenous
30   diabetes-mediating protein genes ablated. Generally, the transgenic mammal will have the transgenic gene under control of an insulin, CMV, interferon, or MHC promoter. In further specific embodiments, a transgenic mammal expresses elevated levels of an endogenous diabetes-mediating gene obtained by an enhanced promoter or a high copy number of an endogenous diabetes-mediating gene. In further specific embodiments, the transgenic
35   mammal has a disrupted diabetes-mediating protein gene.

        The invention further includes mammals in which an endogenous diabetes-mediating protein gene is exogenously altered by methods known in the art, for example, by application of gene activation technologies such as that described in U.S. Patent No. 5,641,670, entirely incorporated herein by reference.

In one aspect, the invention features an assay for screening compounds which effect the expression of one or more diabetes-mediating proteins. In one embodiment, animals at risk for spontaneous development of diabetes are used in an assay for determining the ability of a test compound to effect the expression of one or more diabetes-mediating protein(s). In a preferred embodiment, the assay animal is the transgenic mammal of the invention having a high risk of the development of diabetes. By the term "effect the expression of a diabetes-mediating protein" is meant a compound which induces, enhances, inhibits, or decreases the expression of an endogenous diabetes-mediating protein.

In specific embodiments, the invention provides an assay for identifying a compound capable of inducing or enhancing the expression of an endogenous protective protein, and thus to delay or inhibit the development of diabetes. In another specific embodiment, the assay method of the invention is useful for identifying a compound capable of suppressing or inhibiting the expression of a deleterious diabetes-mediating protein, thus delaying or inhibiting the development of diabetes.

In a related aspect, the invention provides an assay for identifying a compound which modulates the activity of a diabetes-mediating protein, e.g., an agonist, an antagonist, or by blocking a post-translational step required for activation of a diabetes-mediating protein. Changes in the expression of specific DM proteins are useful in a screening method for identifying compounds capable of modulate the expression of DM proteins. A compound which modulates the expression of one or more diabetes mediating proteins is useful as a potential therapeutic in the treatment or prevention of diabetes. Accordingly, in one aspect the invention features an assay method for identifying compounds capable of modulating the expression of diabetes-mediating proteins having the steps of contacting a test compound with a cell or tissue expressing one or more diabetes-mediating proteins, and determining the effect of the test compound on the expression of one or more diabetes-mediating proteins. Determination of the effect of a compound may be conducted by a variety of methods known to the art, including hybridization to probes or other oligonucleotides, antibody recognition, e.g., immunodiffusion, immunofluorescence, ELISA, RIA, blotting, immunoprecipitation, immunoelectrophoresis, or chromatography, and electrophoresis. A compound capable of increasing the expression of one or more proteins selected from the group consisting of the diabetes-mediating proteins listed in Tables 1 and 2 and decreasing the expression of one or more proteins selected from the list consisting of the diabetesmediating proteins listed in Tables 1 and 2 is a candidate therapeutic agent for the prevention or treatment of diabetes. Changes in protein expression are determined relative to expression in the absence of the test compound.

In another aspect, the invention provides a therapeutic method for preventing diabetes in a subject at risk for diabetes or of ameliorating the symptoms of diabetes in a diabetic subject by administering a therapeutically effective amount of a protective

diabetes-mediating protein. Preferably the subject is a human. Also included in the invention is gene therapy by providing a polynucleotide encoding a protective diabetes-mediating protein. The invention further includes a therapeutic method for preventing and/or treating diabetes by administering an effective amount of a polynucleotide which inhibits the *in vivo* expression of a deleterious diabetes-mediating protein. Candidate therapeutic compounds are selected from the proteins of Tables 1 and 2.

In a related aspect, the invention provides a therapeutic method of preventing and/or treating diabetes in a subject at risk for diabetes by administering a therapeutically effective amount of a compound capable of suppressing or reducing the expression of an endogenous deleterious diabetes-mediating protein. In another embodiment, the invention provides a therapeutic method of preventing and/or treating diabetes by administering a therapeutically effective amount of a compound capable of inducing or enhancing the expression of an endogenous protective diabetes-mediating protein. In a related aspect, the invention provides a therapeutic method of preventing and/or treating diabetes in a subject at risk for diabetes by administering a therapeutically effective amount of a compound capable of modulating the activity of a diabetes-mediating protein, e.g., as an agonist, an antagonist, or by preventing the activation of a diabetes-mediating protein. The therapeutic method of the invention includes *ex vivo* methods known to the art for providing the therapeutic agent to a subject in need thereof.

An object of the invention is to identify proteins which mediate diabetes onset.

An object of the invention is to provide an *in vivo* assay for identification of diabetesmediating proteins.

Another object of the invention is to provide diabetes-mediating proteins which are useful in assays for identifying test compounds capable of preventing, delaying, or ameliorating diabetes in a subject.

Another object of the invention is to provide transgenic animals useful in assays to identify protective or deleterious diabetes-mediating proteins.

Another object of the invention is to provide transgenic animals useful in assay to identify test compounds capable of affecting the expression of a diabetes-mediated protein.

Another object of the invention is to provide a transgenic host mammal (which is small, e.g., less than 1 kg when full grown, and inexpensive to maintain) such as a mouse, rat or hamster which includes a natural, or partially or wholly artificial diabetes-mediating gene.

An advantage of the present invention is that the transgenic mammal can be used to identify a protective protein which can prevent or inhibit disease development in a manner which is substantially faster, more efficient and cheaper than presently available assay methods.

Another advantage is that transgenic mammal can be used as test animals for testing drugs for efficacy in the treatment of humans suffering from diabetes or at risk for the development of diabetes.

Another object of the invention is to provide an assay for identification of test compounds which effect the expression of a diabetes-mediating protein and which are capable of preventing the onset of diabetes in a subject at risk for development of the disease, or for ameliorating the symptoms of diabetes in a diabetic subject.

These and other objects, advantages, and features of the invention will become apparent to those persons skilled in the art upon reading the details of the diabetes-mediating gene(s) and protein(s), assay method, and transgenic mouse as more fully described below, and from the claims.

Brief Description of the Figures

FIGs. 1A and 1B show a fluorograph of a 2-dimensional gel of proteins expressed in neonatal rat islet cells incubated for 24 h in RPMI 1640 + 0.5% normal human serum, followed by a 4 h labeling with [^{35}S]-methionine. FIG. 1A is the isoelectric focusing gel (IEF; pH 3.5-7). FIG. 1B is the non-equilibrium pH-gradient electrophoresis gel (NEPHGE; pH 6.5-10.5). Arrows mark 105 diabetes-mediating proteins.

FIG. 2 is the amino acid sequence of murine mortalin.

FIG. 3 is the amino acid sequence of human mortalin.

FIG. 4 is the amino acid sequence of rat galectin.

FIG. 5 is the amino acid sequence of human galectin.

FIG. 6 is the mass spectroscopy spectrum for diabetes-mediating protein GR75 (mortalin), IEF Spot No. 340, determined using the parameters indicated on the figure legend.

FIG. 7 is the mass spectroscopy spectrum for diabetes-mediating protein, tentatively identified as lamin a, IEF Spot No. 655, determined as indicated.

FIGs. 8-10 are the mass spectroscopy spectrum for a diabetes-mediating, tentatively identified as pyruvate kinase, NEPHGE Spot No. 1, determined as indicated.

FIG. 11 is the mass spectroscopy spectrum for a diabetes-mediating, tentatively identified as 6-phosphobructose-2-kinase, NEPHGE Spot No. 169, determined as indicated.

FIG. 12 is the mass spectroscopy spectrum for a diabetes-mediating, tentatively identified as triose phosphate isomerase, NEPHGE Spot No. 334, determined as indicated.

FIG. 13 is the mass spectroscopy spectrum for a diabetes-mediating, tentatively identified as fructose-biphosphase aldolase, NEPHGE Spot No. 668, determined as indicated.

FIGs. 14-15 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "IEF Spot No. 665," having a molecular weight of 42,243 daltons and a pI of 5.82, determined as indicated.

FIG. 16 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed, "IEF Spot No. 939," having a molecular weight of 25,851 daltons and a pI of 5.09, determined as indicated.

FIGs. 17-18 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "IEF Spot No. 941" having a molecular weight of 22,704 daltons and a pI of 5.15, determined as indicated.

FIG. 19 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "IEF Spot No. 950," having a molecular weight of 25,753 daltons and a pI of 4.53, determined as indicated.

FIGs. 20-23 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "IEF Spot No. 1196" having a molecular weight of 143,064 daltons and a pI of 5.41, determined as indicated.

FIG. 24 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 7," having a molecular weight of 65,522 daltons and a pI of 7.28, determined as indicated.

FIG. 25 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 9," having a molecular weight of 115,709 daltons and a pI of 8.33, determined as indicated.

FIG. 26 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 102," having a molecular weight of 63,560 daltons and a pI of 7.26, determined as indicated.

FIG. 27 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 123," having a molecular weight of 57,040 daltons and a pI of 8.17, determined as indicated.

FIG. 28 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 129," having a molecular weight of 57,609 daltons and a pI of 7.72, determined as indicated.

FIG. 29 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 130," having a molecular weight of 55,734 daltons and a pI of 8.07, determined as indicated.

FIGs. 30-31 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 174," having a molecular weight of 53,830 daltons and a pI of 7.92, determined as indicated.

FIGs. 32-33 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No.181," having a molecular weight of 49,422 daltons and a pI of 7.40, determined as indicated.

FIGs. 34-35 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No.182," having a molecular weight of 54,098 daltons and a pI of 7.61, determined as indicated.

FIG. 36 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No.211," having a molecular weight of 47,925 daltons and a pI of 7.28, determined as indicated.

FIG. 37 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No.231," having a molecular weight of 44,362 daltons and a pI of 8.34, determined as indicated.

FIG. 38 is the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No.236," having a molecular weight of 43,162 daltons and a pI of 7.90, determined as indicated.

FIGs. 39-40 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No.253," having a molecular weight of 39,106 daltons and a pI of 9.05, determined as indicated.

FIG. 41 is a mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "IEF Spot No. 831," having a molecular weight of 34,600 daltons and a pI of 4.76, determined as indicated.

FIGs. 42-43 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "IEF Spot No.949," having a molecular weight of 26,800 daltons and a pI of 4.49, determined as indicated.

FIGs. 44-46 are the mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No.129," having a molecular weight of 57,600 daltons and a pI of 7.72, determined as indicated.

FIG. 47 is a mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 310," having a molecular weight of 35,800 daltons and a pI of 7.57, determined as indicated.

FIG. 48 is a mass spectroscopy spectrum for a novel diabetes-mediating protein, termed "NEPHGE Spot No. 326," having a molecular weight of 34,500 daltons and a pI of 8.62, determined as indicated.

Detailed Description of the Preferred Embodiments

Before the present diabetes-mediating proteins and genes, assay methodology, and transgenic used in the assay are described, it is to be understood that this invention is not limited to particular assay methods, diabetes-mediating proteins and genes, test compounds, or transgenic mammals described, as such methods, genes, preparations, and animals may, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be

limiting, since the scope of the present invention will be limited only by the appended claims.

As used in this specification and the appended claims, the singular forms "a", "an", and "the" include plural references unless the context clearly dictates otherwise. Thus, for example, references to "diabetes-mediating protein" or "a diabetes-mediating protein" include mixtures of such diabetes-mediating proteins, reference to "the formulation" or "the method" includes one or more formulations, methods, and/or steps of the type described herein and/or which will become apparent to those persons skilled in the art upon reading this disclosure and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

Definitions

The term **"protein"** includes proteins, polypeptides, and peptides which are chains of amino acids, including all post-translational modifications (e.g., processing and truncations, glycosylations or phosphorylations) which often play decisive roles in modulating protein function. The term also encompasses natural proteins as well as synthetic or recombinant proteins, polypeptides, and peptides.

The term **"diabetes"** includes insulin-dependent diabetes melitis (IDDM) and type I diabetes. The term **"diabetes-related diseases"** includes such conditions as obesity, circulatory deficiencies, insulin-resistance, syndrome X, diabetic retinopathy, diabetic neuropathy, and the involvement of advanced glycation end products (AGE) in neuropathy and atherosclerosis.

The term **"diabetes-mediating protein"** means a protein which is involved in the development of diabetes. A diabetes-mediating protein is a protein which exhibits an altered expression during the development of diabetes, that is, a protein which is up- or down-regulated, or whose expression is modulated up or down, during the development of diabetes, as compared to the expression of the same protein in the absence of the development of diabetes. A diabetes-mediating protein also means a protein that is modified as associated with the development of diabetes or diabetes-related diseases.

Further, interleukin 1α (IL-1α) is expected to have a detrimental effect on the insulin secreting islets of Langerhans, both *in vivo* and *in vitro* and is considered to play a major role in the development of diabetes. Tthe treatment of islets causes the modulation of 106 proteins, up or down regulating their expression. For the purposes of this invention, the term "diabetes mediating protein" is defined to also include all the proteins (and all of their

modification products) which have been demonstrated to be modulated by IL-α in rat islets *in vitro*, as further described in U.S. provisional application Nos. 60/029,324 (filed October 25, 1996), 60/030,186 (filed November 5, 1996) and 60/030,088 (filed November 5, 1996), the entire contents of which are incorporated herein by reference.

The term "**protein modification**" includes any change in structure (*i.e.*, a qualititive change) of a protein. Such modifications can include, but are not limited to, changes in the amino acid sequence, transcriptional or translational splice variation, pre- or post-translational modifications to the DNA or RNA sequence, addition of macromolecules or small molecules to the DNA, RNA or protein, such as peptides, ions, vitamins, atoms, sugar-containing molecules, lipid-containing molecules, small molecules and the like, as well-known in the art.

One type of protein modification according to the present invention is by one or more changes in the amino acid sequence (substitution, deltion or insertion). Such changes could include, at one or more amino acids, a change from a charged amino acid to a different charged amino acid, a non-charged to a charged amino acid, a charged amino acid to a non-charged amino acid (*e.g.*, giving rise to difference in pI or possibly molecular weight). Any other change in amino acid sequence is also included in the invention. The overall positional change in a gel of a modified protein with a changed amino acid sequence also depends on how many overall charges there are in the protein, as known in the art. Changes in the resolution of the gel (*e.g.*, changing the pH or other gradient component) of the gel can allow detection of minor or major amino acid sequence changes. The type of analysis can also affect how changes are detected, *e.g.*, using sequencing, mass spectrometry, labeled antibody binding,

Another type of modification is by change in length, conformation or orientation in the protein-encoding DNA or RNA that affects the way the open reading frame is read in the cell, which can give large changes in position of the spot on the gel and which could affect the analysis of the protein type and position in the gel.

Another typd of protein modification is by changes in processing of the protein in the cell. A non-limiting example is where some proteins have an "address label" specifiying where in (or outside of) the cell they should be used. Such a label or tag can be in the form of a peptide, a sugar or a lipid, which when added or removed from the protein, determines where the protein is located in the cell.

A further type of protein modification is due to the attachment of other macromolecules to a protein. This group can include, but is not limited to, any addition/removal of such a macromolecule. These molecules can be of many types and can be either permanent or temporary. Examples include: (i) polyribosylation, (ii) DNA/RNA (single or double stranded); (iii) lipids and phosphlipids (e.g., for membrane attachment); (iv) saccharides/polysaccharides; and (v) glycosylation (addition of a multitude of different

types of sugar and sialic acids -- in a variety of single and branched structures so that the number of variations possible is large).

Another type of protein modification is due to the attachment of other small molecules to proteins. Examples can include, but are not limited to: (i) phosphorylation; (ii) acetylation; (iii) uridylation; (iv) adenylation; (v) methylation, and (vi) capping (diverse complex modification of the N-terminus of the protein for assorted reasons). Most of these changes are often used to regulate a protein's activity. (v) and (vi) are also used to change the half-life of the protein itself. These protein changes can be detected by 2D using several methods, such as labeling, changes in pI, antibodies or other specific techniques directed to the molecules themselves, as known in the art. Molecular weight changes can be, but may not usually be detectable by 2DGE. MALD (matrix assisted laser desorption of flight mass spectrometry) is preferred to detect and characterize these modifications.

The term "expression" is meant to include not only the physical expression of a protein, but also as a measure of the activity of an expressed protein. For example, a protein can be expressed as an inactive form, which is activated by phosphorylation. While the actual expression of the protein has not changed, its effective expression (activity) has been modified. On a gel, the change in activity may be measured as the change in expression of a modified form of the protein.

The term "affected protein" means a protein that is modified in expression or modified structurally. An affected protein can thus be a protein in which expression is modified due to treatment with one or more compounds, a diseased or pathological state and/or an immunological change in or outside the cell from which the protein is derived. An affected protein can alternatively or additionally also be a protein which exhibits an altered expression as up- or down-regulated, or whose expression is modified in structure in any way that can be detected by a method of the present invention, as compared to the the expression of the same protein (*i.e.*, an "unaffected protein") in the absence of such treatment, disease or immunological change.

The term "diabetes-mediating gene or polynucleotide" means genetic material encoding a protein, peptide, or protein fragment which encodes an intact or fragment of a diabetes-mediating protein. The term includes any gene from any species which encodes a diabetes-mediating protein. A diabetes-mediating gene or polynucleotide may be naturally occurring or partially or wholly synthetic.

The term "substantially pure," when referring to a polypeptide, means a polypeptide that is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. A substantially pure diabetes-mediating protein is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, diabetes-mediating protein. A substantially pure diabetes-mediating protein can be obtained, by extraction from a natural source; by expression of a recombinant nucleic acid encoding a diabetes-mediating protein, or by chemically

synthesizing the protein. Purity can be measured by any appropriate method, e.g., column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

As used herein, "polynucleotide" refers to a nucleic acid sequence of deoxyribonucleotides or ribonucleotides in the form of a separate fragment or a component of a larger construct. DNA encoding portions or all of the polypeptides of the invention can be assembled from cDNA fragments or from oligonucleotides that provide a synthetic gene which can be expressed in a recombinant transcriptional unit. Polynucleotide sequences of the invention include DNA, RNA, and cDNA sequences, and can be derived from natural sources or synthetic sequences synthesized by methods known to the art.

As used herein, an "isolated" polynucleotide is a polynucleotide that is not immediately contiguous (i.e., covalently linked) with either of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome of the organism from which the polynucleotide is derived. The term therefore includes, for example, a recombinant polynucleotide which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequences.

The isolated and purified polynucleotide sequences of the invention also include polynucleotide sequences that hybridize under stringent conditions to the polynucleotide sequences specified herein. The term "stringent conditions" means hybridization conditions that guarantee specificity between hybridizing polynucleotide sequences. One skilled in the art can select posthybridization washing conditions, including temperature and salt concentrations, which reduce the number of nonspecific hybridizations such that only highly complementary sequences are identified (Sambrook *et al.* in *Molecular Cloning*, 2d ea.; Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989), hereby specifically incorporated by reference). For instance, such conditions are hybridization under specified conditions, e.g. involving presoaking in 5xSSC and prehybridizing for 1h at about 40°C in a solution of 20% formamide, 5xDenhardt's solution, 50 mM sodium phosphate, pH 6.8, and 50 µg of denatured sonicated calf thymus DNA, followed by hybridization in the same solution supplemented with 100 µM ATP for 18 h at about 40°C (Sambrook *et al.* supra (1989)). The isolated and purified polynucleotide sequences of the invention also include sequences complementary to the polynucleotide encoding a diabetesmediating protein (antisense sequences) and ribozymes.

The terms "host animal" and "host mammal" are used to describe animals into which donor cells are transplanted. Convenient host animals include mice, hamsters and rats.

The terms "ablated diabetes-mediating protein gene", "disrupted diabetes-mediating gene", and the like are used interchangeably herein to mean an endogenous

diabetes-mediating protein gene which has been altered (e.g., add and/or remove nucleotides) in a manner so as to render the gene inoperative. It is also used to include ablation or modification of controlling sequences or regulatory genes which also render the gene inoperative (partially or completely).

The term **"increased risk of developing diabetes"** and the like mean animals which are genetically predisposed to develop diabetes, preferably having a greater than 50% chance, more preferably a greater than 60% chance, even more preferably a greater than 70% chance, even more preferably a greater than 80% chance, and most preferably a greater than 90% chance to develop diabetes.

By **"altered protein"** or **"altered protein expression"** is meant proteins whose expression is increased ("up regulated"), decreased ("down regulated"), inhibited (i.e., turned off), or induced (i.e., turned on) during the development of diabetes.

By the term **"modulating the activity"** or the like is meant altering the activity of a protein to prevent or enhance its normal activity, e.g., as an agonist, antagonist, or by blocking a post-translational modification step required for protein activity.

By the term **"effective amount"** or **"therapeutically effective amount"** is meant an amount of a compound sufficient to obtain the desired physiological effect, e.g., suppression of or delay of the development of diabetes.

The terms **"treatment"**, **"treating"** and the like are used herein to generally mean obtaining a desired pharmacologic and/or physiologic effect. The effect may by prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete cure for a disease and/or adverse effect attributable to the disease. "Treatment" as used herein covers any treatment of a disease in a mammal, particularly a human, and includes:

(a)   preventing the disease from occurring in a subject which may be predisposed to the disease but has not yet been diagnosed as having it;

(b)   inhibiting the disease, i.e., arresting its development; or

(c)   relieving the disease, i.e., causing regression of the disease. The invention is directed to treating patients with or at risk for development of diabetes and related conditions mediated diabetes, insulin insufficiency, or insulin resistance. More specifically, "treatment " is intended to mean providing a therapeutically detectable and beneficial effect on a patient at risk for or suffering from diabetes.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down the development of a disease. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in which the disorder is to be prevented.

The terms **"synergistic"**, **"synergistic effect"** and like are used herein to describe improved treatment effects obtained by combining one or more therapeutic agents. Although a synergistic effect in some field is meant an effect which is more than additive

(e.g., 1+1=3), in the field of medical therapy an additive (1+1=2) or less than additive (e.g., 1+1=1.6) effect may be synergistic. For example, if each of two drugs were to inhibit the development of diabetes by 50% if given individually, it would not be expected that the two drugs would be combined to completely stop the development of diabetes. In many instances, due to unacceptable side effects, the two drugs cannot be administered together. In other instances, the drugs counteract each other and slow the development of diabetes by less than 50% when administered together. Thus, a synergistic effect is said to be obtained if the two drugs slow the development of diabetes by more than 50% while not causing an unacceptable increase in adverse side effects.

Abbreviations used herein include: IDDM = insulin dependent diabetes mellitus; BB-DP = diabetes prone Bio-Breeding rats; NOD = non-obese diabetic mice.

GENERAL ASPECTS OF THE INVENTION

The present invention encompasses several aspects including: (1) diabetes-mediating proteins identified by differential expression in the presence and absence of the development of diabetes; (2) patterns and combinations of DM proteins useful for predicting the development of diabetes and for identifying a compound able to effect a combination of DM proteins in a desired manner; (3) protective diabetes-mediating proteins; (4) deleterious diabetes-mediating proteins; (5) a method to diagnose for the onset or development of diabetes based on the detection of one or more of the DM proteins, their post-translational modification or degradation products in a body fluid; (6) an *in vivo* method for identifying a diabetes-mediating protein; (7) a transgenic mammal containing an exogenous gene encoding a diabetes-mediating protein; (8) a transgenic mammal useful in an *in vivo* assay for identifying protective or deleterious diabetes-mediating proteins; (9) an *in vitro* assay using transduced cultured cells expressing a diabetes-mediating protein useful for identifying protective or deleterious diabetes-mediating proteins; (10) an *in vivo* assay using transduced islet cells expressing a diabetes-mediating protein useful for identifying protective or deleterious diabetes-mediating proteins; (11) an improved animal model for human diabetes, which animal exhibits a high incidence of diabetes within a predictable period of time; (12) *in vivo* assay methods for identifying test compounds capable of inducing or enhancing the expression of one or more protective proteins; (13) *in vivo* assay methods for identifying test compounds capable of inhibiting or reducing the expression of deleterious proteins, (14) methods for treating diabetes and/or preventing or slowing the development of diabetes in a mammal by providing a therapeutically effective amount of a protective diabetes-mediating protein; (15) methods for treating diabetes and/or preventing or slowing the development of diabetes in a mammal by providing a therapeutically effective amount of a compound capable of inducing or enhancing the expression of a protective diabetes-mediating protein or of modulating the activity of a diabetesmediating protein; and (16) methods for treating diabetes and/or preventing or slowing the development of diabetes in a mammal by providing a therapeutically effective

amount of a compound capable of inhibiting or reducing the expression of a deleterious diabetes-mediating protein, or of modulating the activity of a diabetes-mediating protein.

I.   DIABETES-MEDIATING   PROTEINS,   POLYPEPTIDES, POLYNUCLEOTIDES, AND ANTIBODIES.

5   The invention provides diabetes-mediating proteins, that is, proteins identified as involved in or effected during the development of diabetes. Diabetes-mediating proteins are characterized as proteins whose expression is altered during the development of diabetes relative to their expression in the absence of the development of diabetes. The present disclosure identifies diabetes-mediating proteins from a 2-dimensional gel database
10   of pancreatic islet cell proteins. Diabetes-mediating proteins include protective diabetes-mediating proteins and deleterious diabetes-mediating proteins.

The invention provides *in vitro* methods for identifying diabetes-mediating proteins, including by functionally assessment by expression of cloned cDNA as sense or antisense constructs in transfected cells to establish their deleterious or protective role in
15   cytokine-mediated cytotoxicity.   B cells of the islets of Langerhans are specifically sensitive to the toxic effect of cytokines.   It has previously been demonstrated that lipofection of rat β cells with heat shock protein 70 (HSP70) and induction of hemeoxygenase (HO) by exposure to hemin improved *in vitro* survival of cells exposed to IL-1 (Karlsen *et al.* in: *Insulin Secretion and Pancreatic B Cell Research*, ed: P.R. Flatt
20   and S. Lenzen; Smith-Gordon, USA, pp. 499-507 (1994)). Cells may be transfected in a number of ways known to the art, for example, the adenoviral vector method. See, for example, Korbutt *et al. Transplantation Proceedings* 27:3414 (1995); Csete *et al.* 26:756-757 (1994); Becker *et al. J. Biol. Chem.* 269:21234-21238 (1994).

Following establishment of stable transfected β cell clones, the effect of the
25   expression of a diabetes-mediating protein may be determined by functional analysis of the clones cultured in the absence and presence of cytokines. The functional analyses include nitrous oxide production (NO) measured as nitrite (Green *et al. Anal. Biochem.* 126:131-138 (1982)), insulin secretion (Id.), cytotoxicity, and 2D-gel electrophoresis. Cytotoxicity may be measured by a variety of methods known to the art, including (1) a colorimetric
30   assay based on lactate dehydrogenase (LDH) release (CytoTox, Promega), (2) a life-death assay based on calcein uptake and fluorescence of living cells and ethidium bromide staining of the nuclei of dead cells (Molecular Probes), (3) non-radioactive cell proliferation assay (MTT, Promega), apoptosis (Nerup *et al.* in: *IDDM*, S. Baba & T. Kaneko, eds., Elsevier Science, pp. 15-21 (1994)), and/or semiquantitative multiplex PCR
35   analysis of gene expression. 2-dimensional gels can be used to compare control and cytokine stimulated islets to identify which proteins respond, identifying the proteins which play a role in the cell response. Interlink analysis can be used to define functional groups of proteins and their regulation (e.g., by kinase phosphorylation or other post-translational modifications).

Preferred cells for use in the in such an assay are insulin-secreting cells, for example, MSL or RIN cells. The MSL cell line is a pluripotent or stem-cell like metastatic rat insulinoma cell line. Dependent upon culture and/or passage conditions *in vitro* and *in vivo*, the MSL cell can acquire all four hormone secretory phenotypes characteristic of the islets of Langerhans (Mandrup-Poulsen *et al. Eur. J. Endocrinology* 133:660-671 (1995); Id. *Eur. J. Endocrinology* 134:21-30 (1996)). RIN cells are a cultured line of insulinoma cells (Nielsen *Exp. Clin. Endocrinol.* 93:277-285 (1989)).

Protective diabetes-mediating proteins. The invention provides substantially purified protective diabetes-mediating proteins ("**protective proteins**") characterized as capable of protecting against development of diabetes in a subject at risk for the development of the disease or ameliorating or reducing the symptoms of diabetes in a subject suffering from diabetes. The protective protein of the invention may act directly to protect against diabetes, or may act indirectly by inducing or increasing the synthesis of a second protective protein or by reducing or inhibiting the synthesis of a deleterious protein.

In a specific embodiment, the invention provides the substantially pure protective protein galectin-3. The sequence of rat galectin (SEQ ID NO:3) is shown in FIG. 4, and for human galectin (SEQ ID NO:4) in FIG. 5. As shown below, gal-3 expressed in transfected cells increased cell survival upon challenge with IL-1β. Galectins are lectins with specificity for β-galactoside sugars or glycoconjugates which are present in fetal and adult pancreatic islet cells. The term "**substantially pure**" as used herein refers to gal-3 which is substantially free of other proteins, lipids, carbohydrates or other materials with which it is naturally associated. One skilled in the art can purify gal-3 using standard techniques for protein purification. The purity of the gal-3 polypeptide can also be determined by amino-terminal amino acid sequence analysis. The gal-3 protein includes functional fragments of the polypeptide, as long as the protective activity remains. Smaller peptides containing the biological activity of gal-3 are included in the invention. The invention further includes amino acid sequences having at least 80%, preferably 90%, more preferably 95% identity to the fully length amino acid sequence of SEQ ID NO:4. Percent homology or identity can be determined, for example, by comparing sequence information using the GAP computer program, version 6.0, available from the University of Wisconsin Genetics Computer Group (UWGCG). The GAP program utilizes the alignment method of Needleman and Wunsch *J. Mol. Biol.* 48:443 (1970), as revised by Smith and Waterman *Adv. Appl. Math.* 2:482 (1981). Briefly, the GAP program defines similarity as the number of aligned symbols (i.e., nucleotides or amino acids) which are similar, divided by the total number of symbols in the shorter of the two sequences. The preferred default parameters for the GAP program include: (1) a unitary comparison matrix (containing a value of 1 for identities and 0 for non-identities) and the weighted comparison matrix of Gribskov and Burgess *Nucl. Acids Res.* 14:6745 (1986), as described by Schwartz and Dayhoff, eds.

Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, pp. 353-358 (1979); (2) a penalty of 3.0 for each gap and an additional 0.10 penalty for each symbol in each gap; and (3) no penalty for end gaps.

The invention also provides purified proteins identified or characterized by a computer system or method of the present invention, where the protein can be selected from the group consisting of

(a)   unaffected proteins having the corresponding molecular weights and pIs as presented in Table 8;

(b)   affected proteins having the corresponding molecular weights and pIs as presented in Table 9; and

(c)   marker proteins having the corresponding molecular weights and pIs as presented in Table 10,

and wherein said at least one of said proteins is optionally further selected from the group consisting of

(i)   unaffected proteins having the corresponding molecular weights and pIs as presented in Table 11;

(ii)   affected proteins having the corresponding molecular weights and pIs as presented in Table 12; and

(iii)   marker proteins having the corresponding molecular weights and pIs as presented in Table 13.

According to the invention, an affected or unaffected peptide includes an association of two or more polypeptide domains, such as transmembrane, cytoplasmic, hydrophobic, hydrophilic, ligand binding, or pore lining domains, or fragments thereof, corresponding to an affected or unaffected peptide, such as 1-40 domains or any range or value therein.   Such domains of an affected or unaffected peptide of the invention can have at least 74% homology, such as 74-100% overall homology or identity, or any range or value therein to one or more corresponding affected or unaffected protein or peptide domains as described herein. As would be understood by one of ordinary skill in the art, the above configuration of domains are provided as part of an affected or unaffected peptide of the invention, such that a functional affected or unaffected protein or peptide, when expressed in a suitable cell, is capable of the associated biological activity found in that affected islet cell type. Such activity, as measured by suitable affected or unaffected protein or peptide activity assays, establishes affected or unaffected protein or peptide activity of one or more affected or unaffected proteins or peptides of the invention.

Accordingly, an affected or unaffected peptide of the invention alternatively includes peptides having a portion of an affected or unaffected protein or peptide amino acid sequence which substantially corresponds to at least one 20 to 10,000 amino acid fragment and/or consensus sequence of an affected or unaffected peptide, or group of affected or unaffected peptides, wherein the affected or unaffected protein or peptide has

homology or identity of at least 74-99%, such as 88-99% (or any range or value therein, *e.g.*, 87-99, 88-99, 89-99, 90-99, 91-99, 92-99, 93-99, 94-99, 95-99, 96-99, 97-99, or 98-99%) homology or identity to at least one sequence or consensus sequence of at least one protein characterized as presented in one or more of tables 8-13, or as presented in Figures 2-7, having the mass spec characteristics of one or more of proteins according to the present invention.

In one aspect, such an affected or unaffected peptide can maintain affected or unaffected protein or peptide biological activity. It is preferred that an affected or unaffected peptide of the invention is not naturally occurring or is naturally occurring but is in a purified or isolated form which does not occur in nature. Preferably, an affected or unaffected peptide of the invention substantially corresponds to any set of domains of an affected or unaffected protein or peptide of the invention, having at least 10 contiguous amino acids of proteins characterized in one or more of tables 8-13, comprising SEQ ID NOS:, having the mass spec characteristics of one or more of proteins according to the present invention.

Alternatively or additionally, an affected or unaffected peptide of the invention can comprise at least one domain corresponding to known protein domains, such as cytoplasmic, intracellular, transmembrane, extracellular, or other known domains, having 74-100% overall homology or any range or value therein. Alternative domains are also encoded by DNA which hybridizes under stringent conditions to at least 30 contiguous nucleotides encoding at least 10 contiguous amino acids of proteins characterized in one or more of tables 8-13, Figures 2-7, comprising SEQ ID NOS:, having the mass spec characteristics of one or more of of proteins according to the present invention, or at least 74% homology thereto, or having codons substituted therefor which encode the same amino acid as a particular codon. Additionally, phosphorylation (*e.g.*, PKA and PKC) domains, as would be recognized by the those skilled in the art are also considered when providing an affected or unaffected peptide or encoding nucleic acid according to the invention. A non-limiting example of this is presented in proteins 672-674 of table 12, wherein the same protein is differentially phosphorylated.

The invention further includes polynucleotide sequences encoding the diabetes-mediating proteins of the invention, including DNA, cDNA, and RNA sequences. It is also understood that all polynucleotides encoding all or a portion of a diabetes-mediating protein are also included herein, as long as they encode a polypeptide with the diabetes-mediating activity. Such polynucleotides include naturally occurring, synthetic, and intentionally manipulated polynucleotides. For example, such a polynucleotide may be subjected to site-directed mutagenesis. The polynucleotide sequences of the invention also include antisense sequences. Antisense sequences include sequences synthesized with modified oligonucleotides. The polynucleotides of the invention include sequences that are degenerate as a result of the genetic code. There are 20 natural amino acids, most of

which are specified by more than one **codon. Therefore, all degenerate nucleotide sequences are included in the invention as long as the amino acid sequence of the diabetes-mediating polypeptide is encoded by the nucleotide sequence is functionally unchanged.

The DNA sequences of the invention can be obtained by several methods. For example, the DNA can be isolated using hybridization techniques which are well known in the art. These include, but are not limited to: 1) hybridization of genomic or cDNA libraries with probes to detect homologous nucleotide sequences, 2) polymerase chain reaction (PCR) on genomic DNA or cDNA using primers capable of annealing to the DNA sequence of interest, and 3) antibody screening of expression libraries to detect cloned DNA fragments with shared structural features.

Preferably the DNA sequences of the invention is derived from a mammalian organism, and most preferably from a human. Screening procedures which rely on nucleic acid hybridization make it possible to isolate any gene sequence from any organism, provided the appropriate probe is available. Oligonucleotide probes, which correspond to a part of the sequence encoding the protein in question, can be synthesized chemically. This requires that short, oligopeptide stretches of amino acid sequences must be known. The DNA sequence encoding the protein can be deduced from the genetic code, however, the degeneracy of the code must be taken into account. The codon bias of the organism can be taken into account to select the most probable nucleotide triplets. It is possible to perform a mixed addition reaction when the sequence is degenerate. This includes a heterogeneous mixture of denatured double-stranded DNA. For such screening, hybridization is preferably performed on either single-stranded DNA or denatured double-stranded DNA. Hybridization is particularly useful in the detection of cDNA clones derived from sources where an extremely low amount of mRNA sequences relating to the polypeptide of interest are present. In other words, by using stringent hybridization conditions directed to avoid non-specific binding, it is possible, for example, to allow the autoradiographic visualization of a specific cDNA clone by the hybridization of the target DNA to that single probe in the mixture which is its complete complement (Sambrook *et al. Molecular Cloning: A Laboratory Manual*, 2nd Ed.; Cold Spring Harbor Laboratory Press, Plainview, NY (1989)).

The development of specific DNA sequences encoding the diabetes-mediating proteins of the invention can also be obtained by: 1) isolation of double-stranded DNA sequences from the genomic DNA; 2) chemical manufacture of a DNA sequence to provide the necessary codons for the polypeptide of interest; and 3) *in vitro* synthesis of a double-stranded DNA sequence by reverse transcription of mRNA isolated from a eukaryotic donor cell. In the latter case, a double stranded DNA complement of mRNA is eventually formed which is generally referred to as cDNA. Of the three above-noted methods for developing specific DNA sequences for use in recombinant procedures, the isolation of genomic DNA isolates is the least common. This is especially true when it is

desirable to obtain the microbial expression of mammalian polypeptides due to the presence of introns.

The synthesis of DNA sequences is frequently the method of choice when the entire sequence of amino acid residues of the desired polypeptide product is known. When the entire sequence of amino acid residues of the desired polypeptide is not known, the direct synthesis of DNA sequences is not possible and the method of choice is the synthesis of cDNA sequences. Among the standard procedures for isolating cDNA sequences of interest is the formation of plasmid- or phage-carrying cDNA libraries which are derived from reverse transcription of mRNA which is abundant in donor cells that have a high level of genetic expression for the protein of interest. When used in combination with polymerase chain reaction technology, even rare expression products can be cloned. In those cases where significant portions of the amino acid sequence of the polypeptide are known, the production of labeled single or double-stranded DNA or RNA probe sequences duplicating a sequence putatively present in the target cDNA may be employed in DNA/DNA hybridization procedures which are carried out on cloned copies of the cDNA which have been denatured into a single-stranded form (Jay *et al. Nucl. Acid Res.*, 11 :2325 (1983)).

A cDNA expression library, such as lambda gt11, can be screened indirectly for diabetes-mediating peptides having at least one epitope, using antibodies specific for a diabetes-mediating protein. Such antibodies can be either polyclonally or monoclonally derived and used to detect expression product indicative of the presence of the desired cDNA.

DNA sequences encoding a diabetes-mediating can be expressed *in vitro* by DNA transfer into a suitable host cell. "**Host cells**" are cells in which a vector can be propagated and its DNA expressed. The term also includes any progeny of the subject host cell. It is understood that all progeny may not be identical to the parental cell since there may be mutations that occur during replication. However, such progeny are included when the term "host cell" is used. Methods of stable transfer, meaning that the foreign DNA is continuously maintained in the host, are known in the art.

In the present invention, the polynucleotide sequences encoding diabetes-mediating proteins may be inserted into a recombinant expression vector. The term "**recombinant expression vector**" refers to a plasmid, virus or other vehicle known in the art that has been manipulated by insertion or incorporation of the X130 genetic sequences. Such expression vectors contain a promoter sequence which facilitates the efficient transcription of the inserted genetic sequence of the host. The expression vector typically contains an origin of replication, a promoter, as well as specific genes which allow phenotypic selection of the transformed cells. Vectors suitable for use in the present invention include, but are not limited to the T7-based expression vector for expression in bacteria (Rosenberg *et al. Gene* 56:125 (1987)), the pMSXND expression vector for expression in mammalian

cells (Lee and Nathans *J. Biol. Chem.* 263:3521 (1988)) and baculovirus-derived vectors for expression in insect cells. The DNA segment can be present in the vector operably linked to regulatory elements, for example, a promoter (e.g., T7, metallothionein I, or polyhedron promoters).

5   Polynucleotide sequences encoding a diabetes-mediating protein can be expressed in either prokaryotes or eukaryotes. Hosts can include microbial, yeast, insect and mammalian organisms. Methods of expressing DNA sequences having eukaryotic or viral sequences in prokaryotes are well known in the art. Biologically functional viral and plasmid DNA vectors capable of expression and replication in a host are known in the art.
10   Such vectors are used to incorporate DNA sequences of the invention.

           Transformation of a host cell with recombinant DNA may be carried out by conventional techniques as are well known to those skilled in the art. Where the host is prokaryotic, such as *E. coli*, competent cells which are capable of DNA uptake can be prepared from cells harvested after exponential growth phase and subsequently treated by
15   the $CaCl_2$ method using procedures well known in the art. Alternatively, $MgCl_2$ or RbCl can be used. Transformation can also be performed after forming a protoplast of the host cell if desired.

           When the host is a eukaryote, such methods of transfection of DNA as calcium phosphate co-precipitates, conventional mechanical procedures such as microinjection,
20   electroporation, insertion of a plasmid encased in liposomes, or virus vectors may be used. Eukaryotic cells can also be cotransformed with DNA sequences encoding the diabetes-mediating protein of the invention, and a second foreign DNA molecule encoding a selectable phenotype, such as the herpes simplex thymidine kinase gene. Another method is to use a eukaryotic viral vector, such as simian virus 40 (SV40) or bovine papilloma
25   virus, to infect, transform, or transduce eukaryotic cells and express the protein (see, for example, *Eukaryotic Viral Vectors*, Cold Spring Harbor Laboratory, Gluzman ea., 1982).

           Isolation and purification of microbial expressed polypeptide, or fragments thereof, provided by the invention, may be carried out by conventional means including preparative chromatography and immunological separations involving monoclonal or polyclonal
30   antibodies. 2DGE is a preferred method for purification of modifications variants of the proteins from each other.

           Deleterious diabetes-mediating proteins. Deleterious diabetes-mediating proteins ("deleterious proteins") are characterized as enhancing the development of or increasing the risk of a subject developing diabetes. The invention includes substantially purified
35   protective diabetes-mediating proteins, and polynucleotide sequences encoding such proteins. In a preferred embodiment, a deleterious protein is mortalin. The amino acid sequence of murine mortalin (SEQ ID NO:1) is shown in FIG. 2, and of human mortalin (SEQ ID NO:2) in FIG. 3.

Antibodies specific to diabetes-mediatina proteins. The diabetes-mediating proteins of the invention can also be used to produce antibodies which are immunoreactive or bind to epitopes of the diabetes mediating proteins. An antibody may consist essentially of pooled monoclonal antibodies with different epitopic specificities, as well as distinct monoclonal antibody preparations. Monoclonal antibodies are made from antigen containing fragments of the protein by methods well known in the art (Kohler *et al. Nature* 256:495 (1975) ; *Current Protocols in Molecular Biology*, Ausubel *et al.*, ea., 1989).

The term "antibody" as used in this invention includes intact molecules as well as fragments thereof, such as Fab, F(ab')2, and Fv which are capable of binding the epitopic determinant. These antibody fragments retain some ability to selectively bind with its antigen or receptor and are defined as follows:

(1)   Fab, the fragment which contains a monovalent antigen-binding fragment of an antibody molecule can be produced by digestion of whole antibody with the enzyme papain to yield an intact light chain and a portion of one heavy chain;

(2)   Fab', the fragment of an antibody molecule can be obtained by treating whole antibody with pepsin, followed by reduction, to yield an intact light chain and a portion of the heavy chain; two Fab' fragments are obtained per antibody molecule;

(3)   (Fab')2, the fragment of the antibody that can be obtained by treating whole antibody with the enzyme pepsin without subsequent reduction; F(ab')2 is a dimer of two Fab' fragments held together by two disulfide bonds;

(4)   Fv, defined as a genetically engineered fragment containing the variable region of the light chain and the variable region of the heavy chain expressed as two chains; and

(5)   Single chain antibody ("SCA"), defined as a genetically engineered molecule containing the variable region of the light chain, the variable region of the heavy chain, linked by a suitable polypeptide linker as a genetically fused single chain molecule.

Methods of making these fragments are known in the art. See, for example, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York (1988), incorporated herein by reference.

As used in this invention, the term "epitope" means any antigenic determinant on an antigen to which the paratope of an antibody binds. Epitopic determinants usually consist of chemically active surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics.

Antibodies which bind to the diabetes-mediating polypeptides of the invention can be prepared using an intact polypeptide or fragments containing small peptides of interest as the immunizing antigen. The polypeptide or a peptide used to immunize an animal can be derived from translated cDNA or chemical synthesis which can be conjugated to a carrier protein, if desired. Such commonly used carriers which are chemically coupled to

the peptide include keyhole limpet hemocyanin (KLH), thyroglobulin, bovine serum albumin (BSA), and tetanus toxoid. The coupled peptide is then used to immunize the animal (e.g., a mouse, a rat, or a rabbit).

If desired, polyclonal or monoclonal antibodies can be further purified, for example, by binding to and elusion from a matrix to which the polypeptide or a peptide to which the antibodies were raised is bound. Those of skill in the art will know of various techniques common in the immunology arts for purification and/or concentration of polyclonal antibodies, as well as monoclonal antibodies. See, for example, Coligan *et al.* Unit 9, *Current Protocols in Immunology*, Wiley Interscience (1994), herein specifically incorporated by reference.

It is also possible to use the anti-idiotype technology to produce monoclonal antibodies which mimic an epitope. For example, an anti-idiotypic monoclonal antibody made to a first monoclonal antibody will have a binding domain in the hypervariable region which is the "image" of the epitope bound by the first monoclonal antibody.

For purposes of the invention, an antibody or nucleic acid probe specific for a diabetes-mediating protein may be used to detect the diabetes-mediating protein (using antibody) or encoding polynucleotide (using nucleic acid probe) in biological fluids or tissues. The antibody reactive with the diabetes-mediating protein or the nucleic acid probe is preferably labeled with a compound which allows detection of binding to the diabetes-mediating protein. Any specimen containing a detectable amount of antigen or polynucleotide can be used. Further, specific proteins may be selected by their ligands, e.g., galectin-3 binding to lectin-binding protein), and is useful for diagnosis and/or purification of the protein of interest.

When the cell component is nucleic acid, it may be necessary to amplify the nucleic acid prior to binding with a diabetes-mediating protein-specific probe. Preferably, polymerase chain reaction (PCR) is used, however, other nucleic acid amplification procedures such as ligase chain reaction (LCR), ligated activated transcription (LAT) and nucleic acid sequence-based amplification (NASBA) may be used.

II. METHOD FOR IDENTIFYING A DIABETES-MEDIATING PROTEIN

In vivo animal transplantation model. The invention features a method for identifying a diabetes-mediating protein, by providing an *in vivo* assay system which detects proteins which are involved in the development of diabetes or which are specifically effected during development of diabetes. The *in vivo* transplantation assay of the invention described herein allows the identification of proteins involved or effected.

In the method for identifying a diabetes-mediating protein of the invention, insulin-secreting cells or cells capable of developing into insulin-secreting cells are transplanted into a host animal. Transplanted cells are rescued at time points between transplantation and the onset of diabetes, and protein expression determined, and protein expression compared with nontransplanted islets and syngeneic transplants in animals not developing

diabetes. The method of the invention allows proteins exhibiting an altered expression during development of diabetes to be identified. Identified proteins are then isolated and tested further to identification as protective or deleterious diabetes-mediating proteins.

Cells capable of developing into insulin-producing cells include pancreatic islet cells and β cells. Transplanted cells may be obtained from any species of interest, including human cells. A host animal is preferably one which is immunologically compatible with the transplanted cells such that the transplanted cells do not undergo rejection in the host animal.

The host animal may be any animal which develops diabetes and is convenient for study. Preferred host animals are mice, rats and hamsters, with rats and mice being most preferred. In particularly preferred embodiments, the host animal is selected from a strain bred for an increased incidence of diabetes, including BB-DP rats and NOD mice. The method of the invention may also be used with host animals engineered to develop diabetes at a predetermined time, e.g., upon exposure to a specific antigen. See, for example, Oldstone *et al. APMIS* 104:689-97 (1996); von Herrath *et al. J. Clin. Invest.* 98:1324-1331 (1996); Morgan *et al. J. Immunol.* 157:978983 (1996). Other possible host animals include those belonging to a genus selected from Mus (e.g. mice), Rattus (e.g. rats), Oryctolagus (e.g. rabbits), and Mesocricetus (e.g. hamsters) and Cavia (e.g., guinea pigs). In general mammals with a normal full grown adult body weight of less than 1 kg which are easy to breed and maintain can be used.

Method of determining protein expression. Protein expression may be assessed by a variety of means known to the art, including one or two-dimensional gel electrophoresis and immunoblotting.

Two-dimensional gel electrophoresis (2-DGE) is a particularly effective tool for separating mixtures of proteins (Andersen *et al. Diabetes* 44:400-407 (1995)). Cell protein extracts are put onto a gel, and the individual proteins are separated first by charge and then by size. The result is a characteristic picture of as many as 1,000 to 5,000 spots, each usually a single protein. Resolution is improved by increasing gel size, and by enhancing the sensitivity trough the use of radiolabel methods, silver staining, and the reduction in thickness of the gels to 1.5 mm and less.

Method for isolating diabetes-mediating proteins. As described in the Examples below, single proteins recovered from 2D gels can be identified by mass spectrometry to obtain a trypsin cleavage pattern as well as the precise molecular weight of each peptide. These observed values are then used to search in DNA and protein databases to determine if matches exist to previously identified proteins. Identity can be determined from a known protein or deduced from high homology to a known protein. When 2D gel electrophoresis is used to separate and identify protein spots which exhibit an altered synthesis during development of diabetes, an identified protein spot is excised from the gel and digested with trypsin to produce peptides. The peptides are recovered from the gel and subjected

to mass spectroscopy (matrix assisted laser desorption/ionization mass spectrometry)(MALDI) and the resulting MS-profiles are analyzed against the computerized MS-profiles of all sequences found in the public sequence databases, as well as against propriety sequence information. If any matches to previously cloned sequences are obtained, information about the corresponding gene and encoded protein is collected. When an identified diabetes-mediating protein does not match a previously cloned protein, the protein may be microsequenced to obtain partial amino acid sequence information by methods known to the art (see Example 5 below). Based upon results obtained from database searches or amino acid sequencing, specific or degenerate primers are constructed and used to screen rat and human islets libraries or first-strand cDNA by PCR is used to clone partial sequences of the corresponding cDNA. The obtained sequences are then used to obtain full-length coding regions either by 5'-race PCR or by conventional hybridization screening techniques, followed by expression of the recombinant protein (Karlsen *et al. Proc. Natl. Acad. Sci. USA* 88:8337-8341 (1991); Karlsen *et al.* in: *Insulin secretion and pancreatic B-cell research*, Flatt, P.R., ea., Smith-Gordon, USA; Chapter 64, pp. 1-9 (1994); Karlsen *et al. Diabetes* 44:757-758 (1995).

Diabetes-mediating proteins can be isolated in a variety of ways known to the art, including purification from biological material, expression from recombinant DNA (see above). Conventional method steps include extraction, precipitation, chromatography, affinity chromatography, and electrophoresis. For example, cells expressing a diabetes-mediating protein can be collected by centrifugation, or with suitable buffers, lysed, and the protein isolated by column chromatography, for example, on DEAE-cellulose, phosphocellulose, polyribocytidylic acid-agarose, hydroxyapatite or by electrophoresis or immunoprecipitation. Diabetes-mediating proteins may alternatively be isolated by immunoprecipitation with the use of specific antibodies.

III. TRANSGENIC ANIMALS EXPRESSING A DIABETES-MEDIATING PROTEIN TRANSGENE.

In one aspect, the invention includes a transgenic animal containing a gene encoding a diabetes-mediating protein, as well as transgenic animals which are the offspring of a transgenic animal of the invention. The gene encoding a diabetes-mediating protein may be comprised of a naturally occurring or partially or completely of an artificial polynucleotide sequence, i.e. codon sequences not present in the native gene sequence. Transgenic animals containing elevated levels of expression of the diabetes-mediating gene of the invention can be obtained for example, by over-expression of the gene with an enhanced promoter and/or with high copy numbers of the natural gene. Transgenic animals also specifically include a hybrid transgenic animal produced by crossing a transgenic animal with an animal in which one or more diabetes-mediating protein gene(s) are ablated.

Transgenic animals of the invention are useful in a number of ways, including in assays for determining the effect of a candidate protective or deleterious diabetes-mediating protein on the development of diabetes. For example, a transgenic animal carrying a transgene for a candidate protective protein is useful for determining the effect of the expression of the protective transgene on the development of diabetes.

Preferred host animals are mice, rats and hamsters, with rats and mice being most preferred in that there exists considerable knowledge on the production of transgenic animals. Other possible host animals include those belonging to a genus selected from Mus (e.g. mice), Rattus (e.g. rats), Oryctolagus (e.g. rabbits), and Mesocricetus (e.g. hamsters) and Cavia (e.g., guinea pigs). In general mammals with a normal full grown adult body weight of less than 1 kg which are easy to breed and maintain can be used.

The transgenic non-human mammal of the invention (preferably a rat or mouse) will have in some or all of its nucleated cells a gene encoding a diabetes-mediating protein, e.g., one or more of a protection protein or deleterious protein, which gene was introduced into the mammal, or an ancestor of that mammal, at an embryonic or germ cell stage. This "embryonic stage" may be any point from the moment of conception (e.g., as where the sperm or egg bears the foreign gene) throughout all of the stages of embryonic development of the fetus. A "transgenic mammal" as used herein denotes a mammal bearing in some or all of its nucleated cells one or more genes derived from the same or a different species; if the cells bearing the foreign gene include cells of the animal's germline, the gene may be transmissible to the animal's offspring.

Genetics constructs and methodologies of the invention may be used to create animals which due to their genetic make up will develop diabetes and will exhibit symptoms of the disease in a predictable period of time. In a preferred embodiment, the transgenic mammal of the invention exhibits a 80% incidence of diabetes within 70 ± 10 days; more preferably, a 90% incidence of diabetes within 60 ± 5 days; most preferably, a 95% incidence of diabetes within 55 ± 5 days; and even more preferably, a 97% incidence of diabetes within 50 ± 5 days. The animals of the invention are used in assays to test the ability of a candidate protective or deleterious diabetes-mediating protein, or a test compound to prevent, enhance, or slow the development of diabetes.

In one aspect of the invention, genetic constructs and methodologies of the invention are used to create animals having a transgene encoding a candidate protective or deleterious protein. Transgenic animals may be selected from a genetic background predisposed for development of diabetes, or may be double-transgenic animals which will develop diabetes predictable and in a short period of time. In this embodiment of the invention, the animals are used in assays to test the ability of the candidate protective protein to inhibit or reduce the incidence of disease onset. In a related aspect, the animals are used in assays to test the ability of a compound to induce expression of a protective protein and thus to protect the animal from disease development.

In one aspect of the invention, genetics constructs and methodologies of the invention are used to create animals which due to their genetic make up will develop diabetes within a predictable period of time. For example, in one embodiment, transgenic animals are created which express a deleterious diabetes-mediated disease such as mortalin. The animals of the invention are used in assays to test compounds able to prevent or delay the onset of diabetes. In one embodiment, it is preferable to include a deleterious protein gene within the transgenic animal in a relatively high copy number, in that increasing the copy number tends to decrease the time required for disease onset.

Further, adjustments can be made with respect to the use of specific types of enhanced promoters in order to elevate the levels of expression without increasing copy numbers. Specific types of enhanced promoters are known which would provide enhanced expression to the diabetes-mediating protein transgene without increased copy numbers. The enhanced promoters may operate constitutively or inducibly.

The invention also provides a means of creating animal models for diabetes or diabetes related diseases. The transgenic animals of the invention provide a way to develop and test potential therapies for the diabetes, and will eventually lead to cures for this disease.

IV. ASSAYS FOR SCREENING FOR DRUGS CAPABLE OF EFFECTING THE EXPRESSION OF DIABETES-MEDIATING PROTEINS.

Assay methods provided by the invention are useful for screen compounds capable of effecting the expression of a diabetes-mediating protein, and thus the development of diabetes in a mammal. One model for screening drugs capable of effecting the expression of one or more diabetes-mediating proteins is the administration of compounds suspected of having beneficial effects (including antisense oligonucleotides) to cells in culture. Useful cells are RIN, transfected, or islet cells. The effects of the test compound on protein expression may then be assayed by 2D gel electrophoresis.

Another screening model is an *in vivo* method with the use of a mammal at risk for development of diabetes. Briefly, a mammal with an increased risk for diabetes (e.g., diabetes-prone BB rat or NOD mouse) is exposed to a test compound, and the effect of exposure to the test compound on the development of diabetes determined.

The development of diabetes may be monitored throughout the developmental period by determining the expression of one or more diabetes-mediating proteins and comparing by comparing the time of disease onset with expression and timing in the absence of disease development. Determining the expression of one or more diabetes-mediating proteins includes the diabetes-mediating protein itself, a post-translational modification product, and/or diabetesmediating protein degradation product. In one embodiment, activation of a diabetes-mediating protein is determined by measuring the level of the diabetes-mediating protein expression in a test sample. A suitable test sample includes a body fluid, such as blood, urine, or cerebrospinal fluid, or fluid derived from it,

such as plasma or serum. In a specific embodiment, the level of protein expression in a test sample is measured by Western blot analysis. The proteins present in a sample are fractionated by gel electrophoresis, transferred to a membrane, and probed with labeled antibodies specific for the protein(s). In another specific embodiment, the level of diabetesmediating protein expression is measured by Northern blot analysis. Polyadenylated [poly(A)$^+$] mRNA is isolated from a test sample. The mRNA is fractionated by electrophoresis and transferred to a membrane. The membrane is probed with labeled cDNA. In another embodiment, protein expression is measured by quantitative PCR applied to expressed mRNA.

In a more specific embodiment, a mammal capable of developing diabetes is one selected from a strain of mammals which have been bred for an increased incidence of diabetes. Preferable, the mammal is selected from a strain which exhibits a 75% chance of developing diabetes within 69 ± 25 days. More preferably, the mammal is a transgenic mammal of engineered to exhibit a high incidence of diabetes within a predictable period of time. In specific embodiments, the transgenic mammal exhibits a 80% incidence of diabetes within 70 ± 10 days; more preferably, a 90% incidence of diabetes within 60 ± 5 days; most preferably, a 95% incidence of diabetes within 55 ± 5 days; and even more preferably, a 97% incidence of diabetes within 50 ± 5 days.

In yet another aspect, the invention provides for methods for identifying compounds capable of suppressing or reducing the expression of an endogenous deleterious protein, as well as methods for preventing and/or treating diabetes by administering a therapeutically effective among of a compound capable of suppressing or reducing the expression of an endogenous deleterious protein.

The diabetes-mediating proteins of the invention are also useful to screen reagents that modulate diabetes-mediating protein activity. Accordingly, in one aspect, the invention features methods for identifying a reagent which modulates diabetes-mediating protein activity, by incubating a cell expressing a diabetes mediating protein with the test reagent and measuring the effect of the test reagent on diabetes-mediating protein synthesis, phosphorylation, function, or activity. When activation of a diabetes-mediating protein is via phosphorylation, the test reagent is incubated with the diabetes-mediating protein and with either gamma- [labeled-ATP or [^{35}S]-methionine, and the rate of phosphorylation determined. In another embodiment, the test reagent is incubated with a cell transfected with an diabetes-mediating protein polynucleotide expression vector, and the effect of the test reagent on diabetes-mediating protein transcription is measured by Northern blot analysis. In a further embodiment, the effect of the test reagent on diabetes-mediating protein synthesis is measured by Western blot analysis using an antibody to the diabetesmediating protein In still another embodiment, the effect of a reagent on diabetes-mediating protein activity is measured by incubating diabetes-mediating protein with the test reagent, [^{32}P]-ATP, and a substrate in the diabetes-mediating protein pathway. All

experiments would be compared against a normal labeling of cells with [^{35}S]-methionine to determine modulation of protein expression. The rate of substrate phosphorylation is determined by methods known in the art.

The term modulation of diabetes-mediating protein activity includes agonists and antagonists. The invention is particularly useful for screening reagents that inhibit deleterious protein activity. Such reagents are useful for the treatment or prevention of diabetes.

V.   THERAPEUTIC APPLICATIONS

The invention provides methods for preventing and/or treating diabetes in a mammal by administering a therapeutically effective amount of a protective diabetes-mediating protein. Preferably the mammal is a human subject at risk for diabetes.

Drug screening using identified diabetes-mediating proteins and related diabetes therapeutic agents. In a drug-screening assay of the invention, identified protective or deleterious diabetesmediating proteins are used to identify test compounds capable of effecting their expression. Test compounds so identified are candidate therapeutic agents for preventing, ameliorating, or delaying the onset of diabetes in a subject at risk.

A test therapeutic compound which effects the expression of a diabetes-mediating proteins can be, but is not limited to, at least one selected from a nucleic acid, a compound, a protein, an element, a lipid, an antibody, a saccharide, an isotope, a carbohydrate, an imaging agent, a lipoprotein, a glycoprotein, an enzyme, a detectable probe, and antibody or fragment thereof, or any combination thereof, which can be detectably labeled as for labeling antibodies, as described herein. Such labels include, but are not limited to, enzymatic labels, radioisotope or radioactive compounds or elements, fluorescent compounds or metals, chemiluminescent compounds and bioluminescent compounds.

A therapeutic compound is identified in the drug screening assay of the invention through its ability to induce or enhance the expression of a protective protein, such that disease onset is prevented or delayed in a subject at risk for the development of diabetes. A candidate therapeutic compound is also identified by its ability to prevent or decrease the expression of a deleterious protein, such that disease onset is prevented or delayed in a subject at risk for the development of diabetes.

A therapeutic nucleic acid as a therapeutic compound can have, but is not limited to, at least one of the following therapeutic effects on a target cell: inhibiting transcription of a deleterious protein DNA sequence; inhibiting translation of a deleterious protein RNA sequence; inhibiting reverse transcription of an RNA or DNA sequence corresponding to a deleterious protein; inhibiting a post-translational modification of a protein; inducing transcription of a DNA sequence corresponding to a protective protein; inducing translation of an RNA sequence corresponding to a protective protein; inducing reverse transcription of an RNA or DNA sequence corresponding to a protective protein; translation of the nucleic acid as a protein or enzyme; and incorporating the nucleic acid

into a chromosome of a target cell for constitutive or transient expression of the therapeutic nucleic acid.

Therapeutic effects of therapeutic nucleic acids can include, but are not limited to: turning off a defective gene or processing the expression thereof, such as antisense RNA or DNA; inhibiting viral replication or synthesis; gene therapy as expressing a heterologous nucleic acid encoding a therapeutic protein or correcting a defective protein; modifying a defective or underexpression of an RNA such as an hnRNA, an mRNA, a tRNA, or an rRNA; encoding a drug or prodrug, or an enzyme that generates a compound as a drug or prodrug in pathological or normal cells expressing the diabetes-mediating protein or peptide; and any other known therapeutic effects.

Also included in the invention is gene therapy by providing a polynucleotide encoding a protective diabetes-mediating protein.

The invention further includes a method for preventing diabetes by administering an effective amount of a polynucleotide which inhibits the *in vivo* expression of a deleterious diabetes-mediating protein.

In the therapeutic method of the invention, a therapeutic compound is administered to a human patient chronically or acutely. Optionally, a protective protein is administered chronically in combination with an effective amount of a compound that acts on a different pathway than the therapeutic compound. The therapeutic method of the invention can be combined with other treatments for diabetes or with methods for the management of diabetes.

Therapeutic formulations of the therapeutic compound for treating or preventing diabetes are prepared for storage by mixing the compound having the desired degree of purity with optional physiologically acceptable carriers, excipients, or stabilizers (*Remington's Pharmaceutical Sciences*, 16th edition, Oslo, A., Ed., 1980), in the form of lyophilized cake or aqueous solutions. Acceptable carriers, excipients, or stabilizers are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counter ions such as sodium; and/or non-ionic surfactants such as Tween, Pluronics, or polyethylene glycol (PEG). The compound is also suitably linked to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. The amount of carrier used in a

formulation may range from about 1 to 99%, preferably from about 80 to 99%, optimally between 90 and 99% by weight.

The therapeutic compound to be used for *in vivo* administration must be sterile. This is readily accomplished by methods known in the art, for example, by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution. The therapeutic compound ordinarily will be stored in lyophilized form or in solution.

Therapeutic compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The therapeutic compound administration is in a chronic fashion using, for example, one of the following routes: injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial, or intralesional routes, orally or using sustained-release systems as noted below. The therapeutic compound is administered continuously by infusion or by periodic bolus injection if the clearance rate is sufficiently slow, or by administration into the blood stream or lymph. The preferred administration mode is targeted to the tissue of interest (β cell or pancreatic cells) so as to direct the molecule to the source and minimize side effects of the compound.

Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the protein, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (e.g., poly(2-hydroxyethyl-methacrylate) as described by Langer *et al. J. Biomed. Mater. Res.* 15:167-277 (1981) and *Langer Chem. Tech.* 12:98-105 (1982), or poly(vinyl alcohol)), polylactides (U.S. Patent No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al. Biopolymers* 22:547-556 (1983)), non-degradable ethylene-vinyl acetate (Larger *et al.* supra (1981)), degradable lactic acid-glycolic acid copolymers such as the Lupron Depot™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid (EP 133,988).

The therapeutic compound also may be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization (for example, hydroxymethylcellulose or gelatin-microcapsules and poly-[methylmethacylate] microcapsules, respectively), in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nanoparticles and nanocapsules), or in macroemulsions. Such techniques are disclosed in *Remington's Pharmaceutical Sciences*, supra.

While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release molecules for shorter time periods. When encapsulated molecules remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of

biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved, e.g., using appropriate additives, and developing specific polymer matrix compositions.

Sustained-release compositions also include liposomally entrapped therapeutic compound(s). Liposomes containing therapeutic compound(s) are prepared by methods known *per se*: DE 3,218,121; Epstein *et al. Proc. Natl. Acad. Sci.* USA 82:3688-3692 (1985) ; Hwang *et al.Proc. Natl. Acad. Sci.* USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese patent application 83-118008; U.S. Patent Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol% cholesterol, the selected proportion being adjusted for the optimal agonist therapy. A specific example of a suitable sustained-release formulation is in EP 647,449.

An effective amount of therapeutic compound(s) to be employed therapeutically will depend, for example, upon the therapeutic objectives, the route of administration, and the condition of the patient. Accordingly, it will be necessary for the clinician to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect.

If two therapeutic compounds are administered together, they need not be administered by the same route, nor in the same formulation. However, they can be combined into one formulation as desired. Both therapeutic compounds can be administered to the patient, each in effective amounts, or each in amounts that are sub-optimal but when combined are effective. In one embodiment, the administration of both therapeutic compounds is by injection using, *e.g.*, intravenous or subcutaneous means, depending on the type of protein employed. Typically, the clinician will administer the therapeutic compound(s) until a dosage is reached that achieves the desired effect for treatment or prevention of diabetes. For example, the amount would be one which ameliorates symptoms of diabetes and restores normoglycemia. The progress of this therapy is easily monitored by conventional assays.

In specific embodiments of this aspect of the invention, the therapeutic compound is a protective diabetes-mediating gene encodes gal-3, and/or a post-translational modification product of gal-3. A typical daily dosage of a therapeutic compound used alone might range from about 1 µg/kg to up to 100 mg/kg of patient body weight or more per day, depending on the factors mentioned above, preferably about 10 µg/kg/day to 50 mg/kg/day.

Gene therapy. The present invention also provides gene therapy for the treatment of diabetes and diabetes-related disorders, which are improved or ameliorated by a protective polypeptide. Such therapy would achieve its therapeutic effect by introduction of the protective polynucleotide into insulin-producing cells. Delivery of a protective

polynucleotide can be achieved using a recombinant expression vector such as a chimeric virus or a colloidal dispersion system. Especially preferred for therapeutic delivery of sequences is the use of targeted liposomes.

Various viral vectors which can be utilized for gene therapy as taught herein include adenovirus, herpes virus, vaccinia, or, preferably, an RNA virus such as a retrovirus. Preferably, the retroviral vector for *in vitro* cell transformation is a derivative of a murine or avian retrovirus adenovirus. The advantage of adenovirus transduction compared to other transfection methods is the high transfection affectivity and the ability to transfect whole islets. Furthermore, the level of expression can be adjusted by the virus concentration and transduction-time used. Even though the adenovirus-mediated expression is transient, the expression in islets is stable for at least several weeks (Becker *et al. J. Biol. Chem.* 269:21234 (1994); Korbutt *et al. Transplantation Proc.* 27:3414 (1995)).

For stable integration of a transgene into a mammal, a retroviral vector is preferred. Examples of retroviral vectors in which a single foreign gene can be inserted include, but are not limited to: Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), and Rous Sarcoma Virus (RSV). Preferably, when the subject is a human, a vector such as the gibbon ape leukemia virus (GaLV) is utilized. A number of additional retroviral vectors can incorporate multiple genes. All of these vectors can transfer or incorporate a gene for a selectable marker so that transduced cells can be identified and generated. By inserting a diabetes-mediating protein sequence of interest into the viral vector, along with another gene which encodes the ligand for a receptor on a specific target cell, for example, the vector is now target specific. Retroviral vectors can be made target specific by attaching, for example, a sugar, a glycolipid, or a protein. Preferred targeting is accomplished by using an antibody to target the retroviral vector. Those of skill in the art will know of, or can readily ascertain without undue experimentation, specific polynucleotide sequences which can be inserted into the retroviral genome or attached to a viral envelope to allow target specific delivery of the retroviral vector containing the protective polynucleotide.

Since recombinant retroviruses are defective, they require assistance in order to produce infectious vector particles. This assistance can be provided, for example, by using helper cell lines that contain plasmids encoding all of the structural genes of the retrovirus under the control of regulatory sequences within the LTR. These plasmids are missing a nucleotide sequence which enables the packaging mechanism to recognize an RNA transcript for encapsidation. Helper cell lines which have deletions of the packaging signal include, but are not limited to ψ2, PA317 and PA12, for example. These cell lines produce empty virions, since no genome is packaged. If a retroviral vector is introduced into such cells in which the packaging signal is intact, but the structural genes are replaced by other genes of interest, the vector can be packaged and vector virion produced.

Alternatively, NIH 3T3 or other tissue culture cells can be directly transfected with plasmids encoding the retroviral structural genes *gag*, *pol* and *env*, by conventional calcium phosphate transfection. These cells are then transfected with the vector plasmid containing the genes of interest. The resulting cells release the retroviral vector into the culture medium.

Another targeted delivery system for protective polynucleotides is a colloidal dispersion system. Colloidal dispersion systems include macromolecule complexes, nanocapsules, microspheres,beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preferred colloidal system of this invention is a liposome. Liposomes are artificial membrane vesicles which are useful as delivery vehicles *in vitro* and *in vivo*. It has been shown that large unilamellar vesicles (LW), which range in size from 0.2-4.0 μm can encapsulate a substantial percentage of an aqueous buffer containing large macromolecules. RNA, DNA and intact virions can be encapsulated within the aqueous interior and be delivered to cells in a biologically active form (Fraley, *et al. Trends Biochem. Sci.* 6:77 (1981)). In addition to mammalian cells, liposomes have been used for delivery of polynucleotides in plant, yeast and bacterial cells. In order for a liposome to be an efficient gene transfer vehicle, the following characteristics should be present: (1) encapsulation of the genes of interest at high efficiency while not compromising their biological activity; (2) preferential and substantial binding to a target cell in comparison to non-target cells; (3) delivery of the aqueous contents of the vesicle to the target cell cytoplasm at high efficiency; and (4) accurate and effective expression of genetic information (Manning *et al. Biotechniques* 6:682 (1988)).

The composition of the liposome is usually a combination of phospholipids, particularly high-phase-transition-temperature phospholipids, usually in combination with sterols, especially cholesterol. Other phospholipids or other lipids may also be used. The physical characteristics of liposomes depend on pH, ionic strength, and the presence of divalent cations.

Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidyl-glycerol, phosphatidylcholine, phosphatidylserine, phosphatidylethanolamine, sphingolipid, cerebrosides, and gangliosides. Particularly useful are diacylphosphatidyl-glycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and is saturated. Illustrative phospholipids include egg phosphatidylcholine, dipalm itoylphosphatidylcholine and distearoylphosphatidylcholine.

The targeting of liposomes can be classified based on anatomical and mechanistic factors. Anatomical classification is based on the level of selectivity, for example, organ-specific, cell-specific, and organelle-specific. Mechanistic targeting can be distinguished based upon whether it is passive or active. Passive targeting utilizes the natural tendency of liposomes to distribute to cells of the reticulo-endothelial system (RES) in organs which

contain sinusoidal capillaries. Active targeting, on the other hand, involves alteration of the liposome by coupling the liposome to a specific ligand such as a monoclonal antibody, sugar, glycolipid, or protein, or by changing the composition or size of the liposome in order to achieve targeting to organs and cell types other than the naturally occurring sites of localization.

The surface of the targeted delivery system may be modified in a variety of ways. In the case of a liposomal targeted delivery system, lipid groups can be incorporated into the lipid bilayer of the liposome in order to maintain the targeting ligand in stable association with the liposomal bilayer. Various linking groups can be used for joining the lipid chains to the targeting ligand.

Due to the biological activity of therapeutic compounds in enhancing synthesis of secondary therapeutic compounds, there are a variety of applications using the polypeptide or polynucleotide of the invention, including application to disorders related to the expression of such secondary proteins.

The invention provides methods for treatment of diabetes and diabetes-related disorders, which are improved or ameliorated by modulation of deleterious diabetes-mediating gene expression or activity. In one specific embodiment of this aspect of the invention, the deleterious diabetes-mediating gene encodes mortalin. The term "modulate" envisions the suppression of expression of mortalin.

Where suppression of a deleterious protein expression is desirable, for example, suppression of mortalin, nucleic acid sequences that interfere with mortalin expression at the translational level can be used. This approach utilizes, for example, antisense nucleic acid, ribozymes, or triplex agents to block transcription or translation of a specific mortalin mRNA, either by masking that mRNA with an antisense nucleic acid or triplex agent, or by cleaving it with a ribozyme.

Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule (Weintraub *Scientific American* 262:40 (1990)). In the cell, the antisense nucleic acids hybridize to the corresponding mRNA, forming a double-stranded molecule. The antisense nucleic acids interfere with the translation of the mRNA, since the cell will not translate a mRNA that is double-stranded. Antisense oligomers of about 15 nucleotides are preferred, since they are easily synthesized and are less likely to cause problems than larger molecules when introduced into the target mortalin-producing cell.

Use of an oligonucleotide to stall transcription is known as the triplex strategy since the oligomer winds around double-helical DNA, forming a three-strand helix. Therefore, these triplex compounds can be designed to recognize a unique site on a chosen gene (Maher *et al. Antisense Res. and Dev.* 1:227 (1991); Helene *Anticancer Drug Design*, 6:569 (1991)).

Ribozymes are RNA molecules possessing the ability to specifically cleave other single-stranded RNA in a manner analogous to DNA restriction endonucleases. Through the modification of nucleotide sequences which encode these RNAs, it is possible to engineer molecules that recognize specific nucleotide sequences in an RNA molecule and cleave it (Cech *J. Amer. Med. Assn.* 260:3030 (1988). A major advantage of this approach is that, because they are sequence-specific, only mRNAs with particular sequences are inactivated.

There are two basic types of ribozymes namely, *tetrahymena*-type (Hasselhoff *Nature* 334:585 (1988)) and "hammerhead"-type. *Tetrahymena*-type ribozymes recognize sequences which are four bases in length, while "hammerhead"-type ribozymes recognize base sequences 11 - 18 bases in length. The longer the recognition sequence, the greater the likelihood that the sequence will occur exclusively in the target mRNA species. Consequently, hammerhead-type ribozymes are preferable to *tetrahymena*-type ribozymes for inactivating a specific mRNA species and 18-based recognition sequences are preferable to shorter recognition sequences.

Blocking mortalin action either with anti-mortalin antibodies or with a mortalin antisense polynucleotide may be useful for slowing or ameliorating diabetes. The above described method for delivering a protective polynucleotide are fully applicable to delivery of an mortalin antagonist for specific blocking of mortalin expression and/or activity when desirable. A mortalin antagonist can be a mortalin antibody, an antisense polynucleotide sequence, or a compound which suppresses or inhibits the expression of mortalin.

Identification and Characterization of Diabetes-Mediating Proteins

High resolution two-dimensional (2D) gel electrophoresis may be used to separate approximately 2500 protein spots, each spot corresponding to a protein according to molecular weight and pI. A computerized 2-D gel database of 1373 WF rat islet proteins has recently been reported (Andersen *et al. Diabetes* 44:400-407 (1995)) with a qualitative reproducibility of 81% (FIGs. 1A-1B). IL-1β has been shown to induce changes in the expression of 82 protein in BB-DP islet cells incubated *in vitro. in vitro* incubation of BB-DP islets taken from animals after the onset of diabetes shows that 33 of the 82 proteins determined to respond to IL-1β show significant changes in expression at the onset of diabetes.

Based on the results of 2D gel analysis and peptide sequencing or mass spectroscopy analysis, several candidate diabetes-mediating proteins have been identified (Table 1) and cloned from rat and human islet cells, including iNOS, mortalin, and galectin-3 (Madsen *et al.* in *Insulin secretion and pancreatic B cell research*, P.R. Flatt & S. Lenzen, eds., Smith-Gordon, USA, pp. 61-68 (1994)). Manganese superoxide dismustase (MnSOD) has been transfected into β-cells and whole islets of Langerhans with the use of adenovirus mediated gene transfer and expression. Transfection include the generation of stable or transiently transfected cells.

Following transfection, subcloning, and establishment of stable RIN clones expressing the coding region or antisense-fractions of the protein of interest under the control of a CMV or insulin promoter, the diabetes-mediating protein of interest is functionally characterized. Preliminary results show a 100% transduction in RIN cells and up to 70% in isolated islets. Initially, the increased or decreased expression of the protein in the transfected cells is characterized *in vitro* by measurement of NO production, insulin secretion, and/or cytotoxicity. Furthermore, cell cycle and mitochondrial activity may be determined by FACS analysis (Mandrup-Poulsen *et al. Diabetes/Metabolism Reviews* 9:295-309 (1993)) and semiquantitative analysis of gene expression characterized by multiplex PCR (Nerup *et al. Anales Espanoles Pediatria* 58:40-41 (1994)). Additionally, secondary cellular effects of the over- or under-expression of the protein as well as posttranslational modification may be characterized by 2D-gel electrophoresis of the transfected cells. This analysis allows a distinction to be made between primary and secondary effects in the IL-1β induced changes in protein expression pattern.

To establish IL-1β induced changes in islet cells, NO production and insulin release were measured in BB-DP islets of Langerhans *in vitro* after IL-1β exposure and high resolution twodimensional gel electrophoresis to detect protein changes resulting from IL-1 exposure (Example 2). NO production and insulin release in control islets was similar to that observed in WF islets. IL-Iβ inhibited NO production 4.4-fold and insulin release 3.4-fold. 2D gel analysis showed that IL-1β changed the expression of 82 proteins - 22 proteins were up-regulated and 60 down regulated.

High resolution 2DGE was also used to detect protein changes in BB-DP islet syngrafts transplanted into 30 day old BB-DP rats (Example 3). In BB-DP islet syngrafts from newly onset diabetic BB-DP rats, but not in WF islet syngrafts, 15 of these 82 proteins were found to change level of expression (Example 4).

The IL-1β induced changes in protein expression *in vitro* were compared to protein changes in the process of disease occurrence in BB-DP islet syngrafts (Example 4) or in BB-DP islet allograft rejection (Example 6). In BB-DP islet syngrafts from newly onset diabetic BB-DP rats, but not in WF islet syngrafts 15 of these 82 proteins were found to change level of expression.

Proteins exhibiting altered expression with diabetes onset in syngrafted islets were further characterized (Example 5). One of the altered protein spots was identified by amino acid sequencing to have high homology to the heat shock 70 protein (mortalin), which has been demonstrated to be involved in cellular mortality and apoptosis following translocation of this constitutively expressed protein from a perinuclear to the cytoplasmic region (Wadhwa *et al. J. Biol. Chem.* 268:6615 and 268:22239 (1993)). Based on the amino acid sequence, mortalin cDNA was cloned from rat and human islet for further characterization of its involvement in diabetes development. Over-expression of mortalin in rat insulinoma (RIN) β cells under a CMV promoter was lethal to β cells.

Another diabetes-mediating protein was identified as galectin-3. Galectin-3 (gal-3) was identified in 2D gels as spots 1S (phosphorylated twice), 16 (phosphorylated once), and 19 (nonphosphoryolated) (Andersen *et al. Diabetes* 44:400-407 (1995)) (Example 5). Gal-3 is a protein involved in islet development and inhibition of apoptosis. Using the nucleotide sequence, gal-3 was cloned from rat and human islets, subcloned and expressed in RIN cells after selection for stable clones. RIN cells expressing gal-3 exhibited an increased metabolic activity and proliferative rate, and became more resistant to the negative effect of cytokines. The *in vivo* effect of gal-3 expression was studied by transplanting 200 neonatal islets to 30 day old diabetes prone Bio-Breeding rats (BB-DP) (Example 8).

Further work using the NIGMS (National Institute of General Medical Science) human/rat somatic cell hybrid mapping panel # 2 and primers from intron 2 of the gal-3 gene, has mapped gal-3 to chromosome 14. Using the same primers, a P1 clone was obtained from GenomeSystems, Inc. to use for FISH. Initial FISH results obtained with 48 measurements showed 6.2% localized to the 14q13 region, 54.2% to the 14q21 region, and 39.6% to the 14q22 region, which indicate a distal location in the 14q21.3 region.

Inducible nitric oxide synthase (iNOS) was cloned (Karlsen *et al. Diabetes* 44:753 (1995)). The iNOS gene was mapped to mouse chromosome 11, which is in the middle of the *idd4* region; a region identified as a diabetes-linked region in the diabetes prone NOD mouse (Gerling *et al. Mammalian Genome* 5:318 (1994)). When expressed as a recombinant protein in fibroblasts, it was found that the recombinant iNOS was enzymatically active.

Manganese superoxide dismutase (MnSOD) was identified as a down regulated protein by 2D gel analysis. The expression of MnSOD was further characterized in β and islet cells *in vitro* and *in vivo* following adenovirus transduction and transplantation. Mitochondrial isocitate dehydrogenase was identified as a diabetes-mediating protein.

Changes in protein expression associated with allograft rejection were also determined. Neonatal BB-DP islet cells transplanted into 30 day old WK rats were retrieved after 12 days, and protein expression determined (Example 6). It was found that BB-DP islet allografts in WK rats but not in WF islet syngrafts 9 of 82 proteins were found to change level of expression.

Both the syn-and allografted BB-DP islets were compared to non-grafted BB-DP islets with regard to the proteins found to change expression levels during IL-1 exposure of the BB-DP islets *in vitro*. To control for protein-changes induced by the grafting procedure, 200 neonatal WF islets were grafted to 30 day old WF rats. Grafts were retrieved 48 days after transplantation corresponding to the mean time of onset of diabetes in the colony and in the syngrafted BB-DP rats. The grafts were processed and analyzed as described for comparison with WF control islets with regard to the 105 proteins previously found to be changed during IL-1 incubation. This was done to identify protein

changes inducible both by IL-1 and islet syngrafting. as well as to identify rejection-specific proteins.

To further determine a potential role of these proteins in the diabetes pathogenesis, and to identify therapeutic compounds and compounds which induce the expression of therapeutic compounds, transgenic animals carrying the gene encoding the candidate protein and able to express the candidate protein under tissue-specific promoters are generated. The transgenic animals of the invention express candidate proteins under specific promoters such as the insulin, amylin, CMV, or HLA promoters.

Initially, a study was conducted to determine the optimal conditions for adenoviral-mediated gene transfer to the islets of Langerhans in the absence of vector-induced toxicity. As described in Example X, adenoviral mediated transduction of islets resulted in dose-dependent efficient gene transfer with stable transgene expression in the absence of toxicity.

EXAMPLES

The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how to make and use the chimeric genes, transgenic mice and assays of the present invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers used (e.g. amounts, temperature, etc.) but some experimental errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, molecular weight is weight average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

EXAMPLE 1. MATERIALS AND METHODS

Reagents. Ketamin was purchased from Park-Davis (Barcelona, Spain), xylazin from Bayer (Leverkusen, Germany), and Temgesic® from Reckitt and Colemann (Hull, UK). RPMI 1640, Hanks' balanced salt solution (HBSS), and DMEM were purchased from Gibco, Paisley, Scotland. RPMI 1640 contained 11 mmol D-glucose, and was supplemented with 20 mM HEPES buffer, 100,000 IU/l penicillin and 100 mg/l streptomycin. Authentic recombinant human IL-1β was provided by Novo Nordisk Ltd. (Bagsvaerd, Denmark) having a specific activity of 400 U/ng.

Other reagents used: 2-mercaptoethanol, bovine serum albumin (BSA), Tris HCl, Tris base, glycine, (Sigma, St. Louis, USA); trichloracetic acid (TCA), phosphoric acid, NaOH, glycerol, n-butanol, bromophenol blue, sodium nitroprusside (SNP), H_3PO_4 and $NaNO_2$ (Merck, Darmstadt, Germany); filters (HAWP 0.25 mm pore size) (Millipore, Boston, USA); RNAse A, DNAse I (Worthington, Freehold, NJ, USA); [^{35}S]-methionine (SJ 204, specific activity:>1.000 Ci/mmol, containing 0.1% 2-mercaptoethanol), Amplify® (Amersham International, Amersham, UK); urea (ultra pure) (Schwarz/Mann, Cambridge, MA, USA); acrylamide, bisacrylamide, TEMED, ammonium persulphate (BioRad, Richmond, CA, USA); ampholytes: pH 5-7, pH 3.5-10, pH 7-9, pH 8-9.5 (Pharmacia,

Uppsala, Sweden); Nonidet P-40 (BDH, Poole, UK); ampholytes: pH 5-7 and sodium
dodecyl sulphate (Serve, Heidelberg, Germany); agarose (Litex, Copenhagen, Denmark);
ethanol (absolute 96%) (Danish Distillers, Aalborg, Denmark); methanol (Prolabo, Brione
Le Blanc, France); acetic acid (technical quality, 99% glacial) (Bie & Berntsen, Arhus,
Denmark) and X-ray film (Curix RP-2) (AGFA).

Animals. Thirty (28-32) day old BB/Wor/Mol-BB2 (BB-DP), Wistar Furth (WF)
and Wistar Kyoto (WK) rats were purchased from Møllegården, Ll. Skensved, Denmark.
At Møllegården and in the animal facilities at the Steno Diabetes Center/Hagedorn
Research Institute (Gentofte, Denmark) the BB-DP rats were housed separately in a
specific pathogen-free environment. All rats were housed under controlled conditions of
light (light on from 6:00 am to 6:00 pm), humidity (60 - 70%) and temperature (20 - 22C°)
from five days prior to transplantation until sacrifice. The rats were offered a standard rat
chow (Altromin, Chr. Petersen A/S, Ringsted, Denmark) and free access to tap water. Four
to five day-old BB-DP and WF rats were picked up at Møllegården in the morning on the
day of islet isolation, and transported in animal transport boxes.

Transplantation procedure and graft retrieval. The neonatal islets were
transplanted under the kidney capsule of 28 - 32 day-old recipient rats under sterile
conditions as previously described (Korsgren *et al.J. Clin. Invest.* 75:509-514 (1990)).
Since diabetes incidence is similar in male and female BB-DP rats (Pries *et al. Frontiers
in Diabetes Research* 8:19-24 (Shafrir, E., ed.), Smith-Gordon, London (1991) both sexes
were equally used. To reduce a possible risk of graft rejection due to any gender-related
incompatibility, male islets were transplanted to male recipients and female islets to female
recipients (Steiner *et al. Electrophoresis* 16:1969-1976 (1995)). Two-hundred (range: 187-
215) islets were handpicked using a 10 ml Transpferpettor (Brand, Germany) pipette. The
islets were allowed to sediment, and as much supernatant as possible was removed prior
to the transplantation of a volume of 1-2 ml. The recipient rats were weighed, and blood
glucose (BG) was measured. The rats were then anesthetized with ketamin (8.75 mg/100
g) and xylazin (0.7 mg/100 g) ip. A small incision was made over the left kidney, the
kidney was lifted forward, and a small incision using a knife was made. A pocket using
a blunt instrument was gently made in the capsule. The islets were placed under the
capsule towards the lower kidney pole. The muscle and skin were sutured, the rats allowed
to recover in a cage in the operating facility and given Temgesic (0.01 mg) sc in the neck
before returning to the animal facility. The rats were given Temgesic twice daily for 3 days
post transplantation. Blood glucose (BG) was measured every third day. The rats were
killed by cervical dislocation and immediately afterwards the grafted kidneys were
removed. The grafts were carefully dissected from the kidneys and capsules under a
microscope and placed in HBSS.

Graft and islet labeling. The grafts were labeled immediately after retrieval.
Cultured islets were labeled after 24 h of incubation with or without IL-1. Grafts and islets

were washed twice in HBSS and labeled for 4 h at 37°C in 200 ml methionine-free
Dulbecco's modified Eagle's medium (DMEM) with 10% NHS dialyzed for amino acids,
and either 330 mCi [35S]-methionine for the grafts or 200 mCi [35S]-methionine for the
islets. To eliminate 2-mercaptoethanol, [35S]-methionine was freeze-dried for at least 4
h before labeling. After labeling, the grafts and islets were washed three times in HBSS,
the supernatant was removed and the tissue immediately frozen at -80°C.

    Sample preparation. The frozen grafts were crushed in a mortar. The grafts and
islets were resuspended in 100 ml DNAse I/RNAse A solution and lysed by freeze-thawing
twice. After the second thawing, the samples were left on ice for 30 min for the digestion
of nucleic acids and then freeze dried overnight. The samples were dissolved by shaking
in 120 ml lysis buffer (8.5 M urea, 2% Nonidet P-40, 5% 2-mercaptoethanol and 2%
ampholytes, pH range 7-9) for a minimum of 4 h.

    Determination of [35S]-methionine incorporation. The amount of [35S]-
methionine incorporation was quantitated by adding 10 mg BSA (0.2 mg/ml H_2O) as a
protein-carrier to 5 ml of a 1:10 dilution of each sample in duplicate, followed by 0.5 ml
of 10% TCA. This was left to precipitate for 30 min at 4°C before being filtered through
0.25 mm HAWP filters. The filters were dried and placed into scintillation liquid for
counting.

    2-D gel electrophoresis. The procedure has been described earlier (O'Farrell *et al.*
Cell 12:1133-1142 (1977)). Briefly, first dimension gels contained 4% acrylamide, 0.25%
bisacrylamide and ampholytes. Equal numbers of counts (106 cpm) of each sample were
applied to the gels. In case of lower amounts of radioactivity it was necessary to regulate
the exposure time of the gel so that comparable total optical densities were obtained. The
samples were analyzed on both isoelectric focusing (IEF; pH 3.5-7) and non-equilibrium
pH-gradient electrophoresis (NEPHGE; pH 6.5-10.5) gels. Second dimension gels
contained 12.5% acrylamide and 0.063% bisacrylamide and were run overnight. After
electrophoresis, the gels were fixed and treated for fluorography with Amplify® before
being dried. The gels were placed in contact with X-ray films and exposed at -70°C for
3 to 40 days. Each gel was exposed for at least 3 time periods to compensate for the lack
of dynamic range of X-ray films.

    Determination of MW and pI. Molecular weights of the proteins were determined
by comparison with standard gels. The pIs for the individual proteins on the gels were
determined by the use of pI calibration kits. Landmark proteins were identified on gels by
one or several of the following techniques: immunoblotting, immunoprecipitation, micro
sequencing or peptide mapping.

    Computer analysis of fluorographs. Computer analysis was performed using the
BioImage® program (version 6.1) on a Sunsparc workstation. First, the fluorographs were
scanned and spots identified and quantitated by the BioImage® program. Next, anchor
points were placed on the gel (same spot in each gel was assigned the same anchor point),

and the computer was asked to match the gels. After computer matching, manual editing was performed to ensure identification, correct matching of computer found spots and quantitation of spots not found initially by the computer program. Finally, data were extracted for calculations in the Quatro Pro® spreadsheet (Borland version 4.0). To avoid the presence of duplicate spots in the IEF and NEPHGE subgroups, overlapping spots in either the basic part of IEF gels or in the acidic part of NEPHGE gels were omitted from analysis.

Statistical analysis. Student's t test was applied and P < 0.01 was chosen as level of significance.

EXAMPLE 2. In vitro NITRITE AND INSULIN DETERMINATIONS

To investigate IL-1 induced protein changes in BB-DP islets, 150 neonatal BB-DP rats islets were incubated for 24 hours with or without 150 pg/ml of IL-1, after which the medium was sampled for nitrite and insulin measurements. Two dimensional gel analysis of the islets was performed as described below, and fluorographs of the islets were analyzed on computer (see below, n=3 for each group) and compared with the previously established protein database of IL-1 exposed WF rat islets.

Islet isolation and culture. Islets from pancreata of four to five day old inbred BB-DP and WF rats were isolated after collagenase digestion as described by Brunstedt *et al.* in *Methods in Diabetes Research*, Vol. 1, Wiley & Sons, New York, pp. 254-288 (1984), specifically incorporated herein by reference. After 4 days of preculture in RPMI 1640 + 10% fetal calf serum, islets were cultured as follows: 150 BB-DP islets were incubated for 24 h in 37°C humidified atmospheric air in 300 ml RPMI 1640 + 0.5% normal human serum (NHS) with or without the addition of 150 pa/ml IL-18. In separate series of experiments, 200 BB-DP or WF islets were incubated for 24 h in 300 ml RPMI 1640 + 0.5% NHS before grafting.

Nitrite and insulin measurements. Nitrite was measured by Griess reagents as previously described (Green *et al. Anal. Biochem.* 126:131-138 (1982)). The detection limit of the assay was 1 mmol/l, corresponding to 2 pmol/islet. The nitrite level of the corresponding medium without islets was subtracted if the value of the islet-free medium was above the detection limit. The experiments were run in the same assay. Intra- and interassay coefficients of variation calculated from 3 points on the standard curve were: 1 mmol/l: 1.6%, 16.3%; 10 mmol/l: 1.6%, 15.3%; 25 mmol/l: 1.5, 17.0%. Insulin was measured by RIA (Yang *et al. Proc. Natl. Acad. Sci.* 93:6737-6742 (1996)). The detection limit was 35 fmol/ml. Intra- and interassay coefficients of variation between 3 known controls were A: 5.4%, 12.5%; B: 3.6%, 10.2%; C: 3.1%, 9.4%.

Results. To ensure comparability in terms of function (accumulated insulin release) and response to IL-1 between BB-DP islets and the WF islets previously used for 2-D gel analysis (Andersen *et al. supra* (1995)), NO production and insulin release were measured after 24 hours of incubation with or without IL-1. The basal insulin release and NO

production were similar to data from WF islets (basal insulin release (WF islets) 3.3 ± 0.5 versus (BB-DP islets) 2.0 ± 1.1 pmol*islet-1*24h-1, basal NO production <2 pmol*islet-1*24h-1, for both BB-DP and WF islets. IL-1 inhibited accumulated islet insulin release by 3.4 fold and increased NO production by 4.4 fold, similarly to results obtained using neonatal WF rat islets (IL-1 induced NO production: (WF islets) 9,29 ± 1,21 versus (BB-DP islets) 8.91 ± 1.05 pmol*islet-1*24 h-1 and insulin release: (WF islets) 1,4 ± 0,3 versus (BB-DP islets) 0,6 ± 0.6 pmol*islet-1*24 h-1,18,19).

Analysis of fluorographs from BB-DP rat islets ± IL-1. In a computer based analysis of two dimensional gels of neonatal BB-DP rat islet homogenates a total of 1815 (1275 IEF and 540 NEPHGE) proteins were found in 3 of 3 12,5 % acrylamide gels. In neonatal BB-DP rat islets incubated with IL-1 for 24 hours, 1721 (1171 IEF and 550 NEPHGE) were found in 3 of 3 gels. IL-1 was found to significantly change the expression level of 82 proteins compared to control islets (p<0.01); 60 proteins were decreased and 22 increased in expression level (p<0.01) (Table 1).

EXAMPLE 3. ANIMAL TRANSPLANTATION MODEL.

Experiment 1. Initially, to create a synchronized model for the investigation of the cellular and molecular events occurring during development of IDDM, 200 neonatal BB-DP rat islets were isolated and transplanted under the kidney capsule of 30 day old BB-DP rats. Blood glucose was measured every third day, and the incidence of diabetes determined.

The rats were sacrificed 7, 12, 23, 37, 48, and 173 days after transplantation or at onset of diabetes (n=6 in each group). Grafts were double stained for insulin and one of the following MHC class I, II, αβ-TCR, CD4, CD8, or ED1. Staining was expressed as percentage of total graft area (insulin) or number of stained cells per mm^2. The host islets *in situ* were stained in the same way and expressed as percent inflamed islets of the total number of islet cells. Statistical analysis was conducted with Spearman Rank Correlation and Mann-Witney.

Results. The incidence of diabetes (75%) or day of onset of diabetes (69 ±25 days) did no differ significantly from non-transplanted BB-DP rats. A 2-3 fold increase in the number of infiltrating cells in both graft and islets in situ was seen days 12 and 37. Forty-eight days after transplantation, the number of cells increased in both graft and islets in situ for the rats developing diabetes (p < 0.04) compared to day 37 in prediabetic and non-diabetic rats at day 48, respectively. Graft insulin staining area was 80-90% in the nondiabetic and 30% of total graft area in the diabetic grafts with an inverse relationship between insulin content and cellular infiltrate. For all cell types and at all timepoints studied, a positive correlation was found between the percentage of infiltrated islets in the host pancreatic slides and the number of infiltrating cells in the graft from the same animals (p = 0.002-0.00001; r = 0.4-0.7).

Experiment 2. 200 neonatal BB-DP rat islets were transplanted under the kidney capsule of 30 day old BB-DP rats. Allogeneic transplantation from Wistar Furth islets to Wistar Kyoto rats was similarly conducted as a control.

The grafted islets did not affect IDDM incidence or time of disease onset. On the day of diabetes onset (78 ± 5 days) and on day 17 in the control WK animals, the grafts were excised for immunohistochemistry and [^{35}S]-methionine labeling.

Results. Immunohistochemical examination of the grafts from diabetic BB rats demonstrated massive inflammation with MHC class I positive cells (1982/mm^2 ± 534), macrophages (661/mm^2 ± 406), T-helper cells (1331/mm^2 ± 321), cytotoxic T-cells (449/mm^2 ± 117), and insulin positive cells reduced to 33-66$ of the transplant. Allogeneic transplant controls showed fibrosis, less infiltration of mononuclear cells, MHC class II positive cells (152/mm^2), MHC class I positive cells (48/mm^2), macrophages (172/mm^2), T-helper cells (254/mm^2), cytotoxic T-cells (42/mm^2), and insulin content of 100% in the remaining cells.

Computerized analysis of 2D gels showed a greater than 2-fold increase in the expression of 18 of the 33 proteins altered *in vitro* by IL-1 exposure. 14 were specific to the syngeneic transplants in the BB-DP animals. 8 proteins specifically changed level of expression.

EXAMPLE 4. CHANGES IN PROTEIN EXPRESSION INDUCED BY DIABETES ONSET.

To investigate protein changes in BB-DP islet syngrafts during disease occurrence, 200 neonatal BB-DP rat islets were grafted to 30 day old BB-DP rats. Grafts were retrieved at onset of diabetes, defined as BG> 14 mmol/l for two consecutive days, n=5, for labeling, two dimensional gel electrophoresis and computer based comparison with non-grafted BB-DP islets.

Analysis of fluorographs from syngeneic islet-grafts from newly onset diabetic BB-DP rats. In BB-DP islet syngrafts from newly onset diabetic BB-DP rats, computer analysis showed 1818 proteins (1259 IEF and 557 NEPHGE) present in 5 of 5 gels. (These data are preliminary proteins present in both islets *in vitro* and grafts changed expression level (64 were increased and 131 decreased in expression level) when compared to control neonatal BB-DP rat islets (p<0.01, data not shown)). Seventy-one of the eighty-two proteins that changed level of expression in BB-DP rat islets after IL-1 incubation *in vitro* were re-identified in the graft. Of the 71 re-identified proteins 33 significantly changed expression levels (4 up- and 29 down-regulated) in the islet syngrafts at onset of diabetes (Table 2).

Analysis of fluorographs from islet WF syngrafts. To control for changes in protein expression caused by the grafting procedure *per se*, WF islet syngrafts were compared to the protein changes caused by IL-1 in WF neonatal islets *in vitro*. Of the 105 proteins that changed expression level in WF islets incubated with IL-I *in vitro*, 89 proteins were re-identified whereas 12 were absent in the WF islet grafts (n=3) when compared to

the WF control islets. Forty-two of the ninety-three re-identified proteins significantly changed level of expression (27 decreased and 15 increased, p<0.01, Table 5). IL-1 induced proteins *in vitro* specifically seen in islet-grafts during disease occurrence or islet-graft rejection. Proteins that were found to change level of expression in islets after IL-1 incubation *in vitro* and not found to significantly change level of expression in syngrafted WF islets were denoted specific for disease occurrence if found in syngrafted BB-DP islets or specific for graft-rejection if found in allografted BB-DP islets to WK rats. In syngrafted BB-DP islets 28 proteins and in allografted BB-DP islets 29 proteins changed level of expression (data not shown). Fourteen proteins specifically changed level of expression in BB-DP syngrafts and 8 in BB-DP allografts in WK rats.

EXAMPLE 5. CHARACTERIZATION OF DIABETES-MEDIATED PROTEINS

Proteins exhibiting IL-1β-induction of synthesis were analyzed by mass spectrometry and microsequencing as described below. Commercially available protein databases were searched for matches, including SWISS-PROT, PIR, NIH, and GENEBANK.

Microsequencing. Protein spots identified by 2DGE as diabetes-mediated proteins were further characterized by being digested with trypsin in the gel, concentrated, HPLC separated, peak sequenced, and partial sequence compared to known sequences, according to known methods.

Results of microsequences are as follows:

Protein 22 (peak 22): A Q Y E E L I A N G (D) (M) (SEQ ID NO:5)

(peak 13): K K P L V Y D E G (K) (SEQ ID NO:6)

Protein 25 (peak 15): L L E X T X X L X (SEQ ID NO:7)

(peak 16): P S L N S X E X (SEQ ID NO:8)

Galectin-3 (peak 22): I E L X E I X (SEQ ID NO:9)

Direct sequencing of one protein (mw 68,700) yielded the following partial sequence: PEAIKGAVVGIDLG (SEQ ID NO: 10) (Table 2: GR75). This protein has high homology to 75kD glucose regulated protein (GR75, Table 2) (PBP74, P66mot, mortalin); is a constitutive member of hsp70 protein family, not heat-inducible; is ubiquitously expressed in different tissues; comprises a 46 residue leader peptide 75kD processed to 66 kD; is found in mitochondria; is associated with cellular mortality and with antigen presentation.

One protein was identified as galectin-3, a 27kD protein which is present in several tissues, and known to have a role as a pre-mRNA splicing factor. The amino acid sequence of human gal-3 is shown in FIG. 5 (SEQ ID NO:4).

Mass spectroscopy. In situ digestion is performed on at least one gel plug including at least one protein spot in at least one gel according to the present invention. Gels are prepared by a modification of the method of Rosenfeld *et al. Anal. Biochem.* 203:173-179 (1992), as described in Fey *et al. Electrophoresis* 18:1-12 (1997), both of

which references are herein specifically incorporated by reference. Briefly, gels are quickly stained and destained. The protein of interest is obtained by cutting a gel band containing the protein with a scalpel and storing in eppendorf tubes with UHQ water at -20°C. The protein is digested by washing the gel plug for at least 1 hour in 40% acetonitrile/60% digestion buffer until the coomassie stain is removed. This wash removes coomassie stain, gel buffers, SDS and salts. If necessary the wash can be repeated. The gel plug is then dried in a vacuum centrifuge for 20-30 min. until the plug shrinks and becomes white on the surface. Drying time depends on the size and thickness of the gel plug. Trypsin (or the enzyme being used is dissolved in digestion buffer and 5 mls added to the gel plug (depending on the amount of the protein in the gel to be analyzed (0.1 mg)). Additional digestion buffer is added until the gel plug is almost covered by buffer in the bottom of the tube, approximately 10 ml. The gel plug is then incubated at 37°C for 6 hours or overnight, then incubated with 70-100 ml 60% acetonitrile/40% water for 2-6 hours to extract the peptides. The extraction may be repeated to increase recovery. The extract is then lyophilized and dissolved in 30% acetonitrile/2%TFA before analyzing by MALDI-MS.

FIGs. 6-48 provide the mass spectroscopic data obtain for the indicated protein of Tables 1 and 2.

EXAMPLE 6. IN VIVO PROTEIN EXPRESSION DURING ALLOGRAFT REJECTION

To investigate protein changes in BB-DP islet allografts during rejection, 200 neonatal BB-DP rat islets were grafted to 30 day old WK rats (n=3). Grafts were retrieved 12 days after transplantation at which time point substantial mononuclear infiltration is expected. The grafts were processed and analyzed as described above.

Analysis of fluorographs from BB-DP islet allografts in WK rats. Twelve days after transplantation mononuclear cell infiltration was observed in the grafts (18), and computer analysis of fluorographs from the BB-DP islet allografts sampled at this time-point showed 1714 (1064 IEF and 650 NEPHGE) proteins present in 3 of 3 gels. The gels of the BB-DP islet allografts were compared to gels of neonatal BB-DP rat islets with regard to the 82 proteins that significantly changed level of expression in the BB-DP islets after IL-1 incubation *in vitro*. Sixty-six of the eighty-two proteins were re-identified. Thirty-three of the sixty-six re-identified proteins were found to change expression levels (28 decreased and 5 increased, p<0.01).

EXAMPLE 7. ESTABLISHMENT OF NON-TOXICITY OF ADENOVIRAL-MEDIATED GENE TRANSFER IN ISLET CELLS.

To determine the optimal conditions for adenoviral-mediated gene transfer to the islets of Langerhans in the absence of vector-induced toxicity, neonatal rat islets were transduced in groups of 25 in triplicate with an adenoviral vector β-galactosidase (AdβGal) at doses of multiplicity of infection (moi) 0, 10, 100, and 1000 pfu per islet. Efficiency of gene transfer was determined by gross inspection and estimated by the percentage of,6-

galactosidase positive cells after islet dispersion at 1, 4, 7, and 10 days post-transduction. Islet toxicity was assessed by measuring accumulated insulin levels at each time-point and by assessing insulin release in response to hyperglycemia at 3 and 10 days.

Results. Efficient dose-dependent gene transfer to the islets was documented at 1, 4, 7, and 10 days post-transduction. At day 1, 8.3%, 34.1%, and 58.6% of cells in dispersed islets expressed transgene at moi 10, 100, and 1,000, respectively. Transgene expression was stable for the duration of the experiment. Insulin accumulation did not differ between transduced and non-transduced islets at each time-point; and accumulated insulin at 10 days expressed as nmol of insulin per islet was 14.3 ± 1.5 at a moi of 0, 15.0 ± 2.6 at a moi of 10, 22.0 ± 7.8 at a moi of 100, and 15.3 ± 1.5 at a moi of 1,000.

Similarly, the insulin secretory response to glucose, obtained by dividing the insulin response to high glucose incubation by the insulin response to low glucose incubation was similar in transduced and non-transduced islets at 3 days at all doses studied (mod 0; 12.7 ± 4.1; moi 10, 14.9 ± 7.9; moi 100, 15.7 ± 0.7; and moi 1,000, 22.3 ± 6.7). The ratios were similar in transduced and non-transduced cells at 10 days post-transduction.

EXAMPLE 8. EXPRESSION OF GALECTIN-3 IN THE SPONTANEOUS DEVELOPMENT OF IDDM.

200 neonatal BB-DP rat islets were transplanted under the kidney capsule of 30 day old BB-DP rats. Grafts retrieved day 7 after transplantation (prediabetic, n=6), at diabetes onset (n=6) or day 174 after transplantation (animals escaping diabetes, n=3) and IL-113 stimulated and non-stimulated neonatal BB-DP islets were labeled with [35S]-methionine and prepared for high-resolution two-dimensional gel electrophoresis.

Each sample was run on isoelectric focusing (IEF, pH 3.5-7) and non-equilibrium pH-gradient electrophoresis (NEPHGE, pH 6.5-10.5). Fluorographs of the gel were analyzed as described above. Changes in expression levels of proteins were considered significant at p values below 0.01 (Student's t-test).

Results. Neonatal BB-DP islets stimulated with IL-1β *in vitro* showed changes in 82 proteins. 97-98% of these proteins were identified in all grafts at all time points. Expression levels of graft proteins compared with non-stimulated normal BB-DP islets *in vitro* showed the following changes: Of the 82 proteins which exhibit increased expression when neonatal islet cells are treated with IL-1β *in vitro*, 42 were increased in the 7 day transplant islets, 31 were increased with diabetes onset, and 14 were increased in animals which did not develop diabetes. Of the proteins increased, 4 of them are only seen at onset of IDDM and not at the timepoints detailed. At day 7, five proteins which do not change with *in vitro* IL-B exposure were observed to change, while 2 proteins were observed to change at the onset of diabetes, and 3 in the animals which did not develop diabetes. Of the proteins observed to change *in vivo* but not *in vitro*, I of these is identified as IDDM specific. Gal-3 expression was significantly down-regulated at day 7 and at onset of

IDDM. In contrast, gal-3 expression was increased in *in vitro* IL-1β stimulated islets and in grafts from animals which did not develop diabetes.

EXAMPLE 9. CYTOKINE INDUCTION OF IL-1 CONVERTING ENZYME (ICE), INDUCIBLE NITRIC OXIDE SYNTHASE (iNOS), AND APOPTOSIS IN INSULIN-PRODUCING CELLS.

The expression of ICE, iNOS, and induction of apotosis was investigated. Rat insulinoma and pluripotent cells lines RIN-SAH and MSL-G2 were cultured 20 hours with a mixture of cytokines (IL-1β, TNFoα, and IFNγ), RNA isolated, and multiplex PCR analysis (27 cycles) with primers against ICE, iNOS, and SP-1 (a general transcription factor used as a housekeeping control gene for normalization) were formed. Results were normalized to SP-1 mRNA expression, and calculated following gel electrophoresis separation and PhosphorImager quantification.

Results. Neither ICE or iNOS expression were detected in control cells. A marked up-regulation to that of the level of the SP-1 gene product was seen in both ICE and iNOS after 20 hours of cytokine exposure. In RIN cells, ICE was produced at 98% and iNOS produced at 97% of SP-1. Whereas neither apoptosis or NOS production were detected in the control cells, cytokine-induced iNOS production was followed by a high increase in apoptosis-frequency and NO production. In RIN cells, accumulated nitrite was measured to be 19.7 ± 0.7 μM after 3 days.

TABLE 1:	ISLET CELL DIABETES MEDIATING PROTEINS WHICH INCREASE UPON IL-18 STIMULATION IDENTIFIED BY 2DGE		
Gel Spot No.	**Gene**	**Protein**	**Database Accession**
IEF 010	Unknown	MWt: 120,500; pI: 7.27	
IEF 011	EF2	ELONGATION FACTOR 2 (EF-2)	P05197
IEF 025	VAT	VACUOLAR ATP SYNTHASE SUBUNIT B, BRAIN ISOFORM (EC 3.6.1.34)	P31408
IEF 028	MMLAMIN11	LAMIN B1 (mouse)	D50080
IEF 083	PYC	PYRUVATE CARBOXYLASE PRECURSOR (EC 6.4.1.1)	P52873
IEF 085	PYC	PYRUVATE CARBOXYLASE PRECURSOR (EC 6.4.1.1)	P52873
IEF 115	Unknown	MWt: 175,200; pI: 5.23	
IEF 145	Unknown	MWt: 133,100; pI: 6.29	
IEF 173	MVP	MAJOR VAULT PROTEIN	Q62667
IEF 186	HS74	HEAT SHOCK 70 KD PROTEIN AGP-2 (mouse)	Q61316
IEF 187	HS74	HEAT SHOCK 70 KD PROTEIN AGP-2 (mouse)	Q61316
IEF 189	Unknown	MWt: 135,100; pI: 4.96	
IEF 194	UBP1	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T (EC 3.1.2.15)	P45974
IEF 201	CALX	CALNEXIN PRECURSOR	P35565
IEF 210	Unknown	MWt: 114,500; pI: 6.40	
IEF 217	Unknown	MWt: 91,300; pI: 6.12	
IEF 225	Unknown	MWt: 83,300; pI: 5.89	
IEF 265	TERA	TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE)	P46462

Gel Spot N .	Gene	Protein	Database Accession
IEF267	HS9B	HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84)	P34058
IEF 276	Unknown	MWt: 107,500; pI: 4.34	
IEF 279	Unknown	MWt: 121,400; pI: 4.20	
IEF 285	Unknown	MWt: 78,300; pI: 6.66	
IEF 289	Unknown	MWt: 73,900; pI: 6.44	
IEF 306	Unknown	MWt: 75,700; pI: 6.20	
IEF 310	SYG	GLYCYL-TRNA SYNTHETASE (EC 6.1.1.14)	P41250
IEF 329	GR78	78 KD GLUCOSE REGULATED PROT. PREC. (GRP 78)	P06761
IEF 329	NCPR	NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4)	P00388
IEF 330	GR75	MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (MORTALIN)	P48721
IEF 342	Unknown	MWt: 83,300; pI: 4.81	
IEF 347	GR78	78 KD GLUCOSE REGULATED PROT. PREC. (GRP 78)	P06761
IEF 354	Unknown	MWt: 70,400; pI: 4.30	
IEF 382	Unknown	MWt: 63,900; pI: 6.35	
IEF 387	TO64	TURNED ON AFTER DIVISION, 64 KD PROT. (TOAD-64)	P47942
IEF 387	TCPG	T-COMPLEX PROTEIN 1, GAMMA SUBUNIT (Mouse/Human)	P80318
IEF 387	COPD	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (Bovine/Human)	P53619

Gel Spot No.	Gene	Protein	Database Accession
IEF 425	HS7C	HEAT SHOCK COGNATE 71kD PROTEIN	P08109
IEF 471	Unknown	MWt: 60,700; pI: 6.08	
IEF 480	Unknown	MWt: 62,000; pI: 5.91	
IEF 483	ER60	PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60)	P11598
IEF 505	Unknown	MWt: 61,500; pI: 5.41	
IEF 506	TCPE	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (Mouse)	P80316
IEF 507	P60	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HSP-60)	P19227
IEF 561	ENOA	ALPHA ENOLASE (EC 4.2.1.11)	P04764
IEF 563	Unknown	MWt: 48,000; pI: 6.20	
IEF 655	LAMA	LAMIN A	S47890
IEF 759	HSU36764	TGF-β RECEPTOR INTERACTING PROTEIN 1 (HUMAN)	U36764
IEF 1081	Unknown	MWt: 63,800; pI: 5.43	
IEF 1196	Unknown	MWt: 143,100; pI: 5.41; Mass spec FIGs. 20-23	
IEF 1342	Unknown	MWt: 53,400; pI: 4.64	
IEF 1356	Unknown	MWt: 147,900; pI: 5.40	
NEPHGE 017	G3P	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH)	P04797
NEPHGE 156	PTB	POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HNRNP I)	Q00438

Gel Spot No.	Gene	Protein	Database Accession
NEPHGE 169	F261	6-PHOSPHOFRUCTO-2 KINASE (EC 2.7.1.105)	P07953
NEPHGE 203	PGK2	PHOSPHOGLYCERATE KINASE (EC 2.7.2.3),	P16617
NEPHGE 269	ANX2	ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN)	Q07936
NEPHGE 269	G3P	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH)	P04797
NEPHGE 298	LEG3	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3)	P08699
NEPHGE 298	Unknown	MWt: 36,400; pI: 8.32	
NEPHGE 668	ALFA	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13) A (MUSCLE)	P05065
NEPHGE 670	Unknown	MWt: 148,700; pI: 8.10	
NEPHGE 672	Unknown	MWt: 132,500; pI: 8.52	
NEPHGE 673	Unknown	MWt: 132,500; pI: 8.46	
NEPHGE 674	Unknown	MWt: 132,500; pI: 8.42	

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TABLE 2:	ISLET CELL DIABETES MEDIATING PROTEINS WHICH DECREASE UPON IL-18 STIMULATION IDENTIFIED BY 2DGE		
Gel Spot No.	**Gene**	**Protein**	**Database Accession**
IEF 015	Unknown	MWt: 75,400; pI: 6.01	
IEF 339	GR78	78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78)	P06761
IEF 340	GR75	MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR (GRP 75)	P48721
IEF 344	GR78	78 KD GLUCOSE REGULATED PROTEIN PRECURSOR (GRP 78)	P20029
IEF 358	Unknown	MWt: 77,000; pI: 4.11	
IEF 436	NEC2	NEUROENDOCRINE CONVERTASE 2 PRECURSOR (EC 3.4.21.94) (NEC 2)	P28841
IEF 441	NEC2	NEUROENDOCRINE CONVERTASE 2 PRECURSOR (EC 3.4.21.94) (NEC2)	P28841
IEF 442	NEC2	NEUROENDOCRINE CONVERTASE 2 PRECURSOR (EC 3.4.21.94) (NEC 2)	P28841
IEF 484	ER60	PROTEIN DISULFIDE ISOMERASE ER60 PRECURSOR (EC 5.3.4.1) (ERP60)	P11598
IEF 510	Unknown	MWt: 54,400; pI: 5.27	
IEF 614	ERP5	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1)	Q63081
IEF 614	ATPB	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34)	P10719
IEF 665	MTA1	METASTASIS-ASSOCIATED PROTEIN MTA-1	Q62599

Gel Spot No.	Gene	Protein	Database Accession
IEF 719	Unknown	MWt: 39,600; pI: 6.55	
IEF 825	Unknown	MWt: 35,000; pI: 5.10	
IEF 831	Unknown	MWt: 34,600; pI: 4.76; Mass spec FIG. 41	
IEF 882	Unknown	MWt: 30,800; pI: 4.94	
IEF 887	Unknown	MWt: 30,800; pI: 4.76	
IEF 895	Unknown	MWt: 28,900; pI: 4.29	
IEF 908	ER31	ENDOPLASMIC RETICULUM PROTEIN ERP31 PRECURSOR (ERP29)	P52555
IEF 908	PMGB	PHOSPHOGLYCERATE MUTASE, BRAIN FORM (EC 5.4.2.1)	P25113
IEF 939	Unknown	MWt: 25,900; pI: 5.09; Mass spec FIGs. 16	
IEF 941	PBP	PHOSPHATIDYLETHANO LAMINE-BINDING PROTEIN (P23K)	P31044
IEF 949	RNU53882	14-3-3 PROTEIN EPSILON ISOFORM	U53882
IEF 949	Unknown	MWt: 26,800; pI: 4.49 Mass spec FIGs. 42-43	
IEF 950	Unknown	MWt: 25,800; pI: 4.53; Mass spec FIGs. 19	
NEPHGE 001	KPY2	PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40)	P11981
NEPHGE 007	Unknown	MWt: 65,500; pI 7.28; Mass spec FIG. 24	
NEPHGE 009	Unknown	MWt: 115,700; pI 8.33; Mass spec FIG. 25	
NEPHGE 018	DHE3	GLUTAMATE DEHYDROGENASE PRECURSOR (EC 1.4.1.3) (GDH)	P10860

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Gel Spot No.	Gene	Protein	Database Accession
NEPHGE 102	TCPZ	T-COMPLEX PROTEIN 1, ZETA SUBUNIT	P80317
NEPHGE 102	RNPKMPS	PYRUVATE KINASE M	M24361
NEPHGE 123	KPY2	PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40)	P11981
NEPHGE 129	KPY2	PYRUVATE KINASE, M2 ISOZYME	P11981
NEPHGE 129	Unknown	MWt: 57,600; pI: 7.72 Mass spec FIGs. 44-46	
NEPHGE 130	MMSA	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE PRECURSOR	Q02253
NEPHGE 130	RNPKMPS	PYRUVATE KINASE M INTRONLESS PROCESSED PSEUDOGENE	M24361
NEPHGE 171	ATPA	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34)	P15999
NEPHGE 174	DHE3	GLUTAMATE DEHYDROGENASE PRECURSOR (EC 1.4.1.3) (GDH)	P10860
NEPHGE 176	ATPA	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34)	P15999
NEPHGE 181	Unknown	MWt: 49,400; pI: 7.40; Mass spec FIGs. 32-33	
NEPHGE 182	DHE3	GLUTAMATE DEHYDROGENASE PRECURSOR (EC 1.4.1.3) (GDH)	P10860
NEPHGE 211	Unknown	MWt: 47,900; pI: 7.28; Mass spec FIG. 36	

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Gel Spot No.	Gene	Protein	Database Accession
NEPHGE 227	THIL	ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9)	P17764
NEPHGE 231	BKCRU	CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL PRECURSOR (EC 2.7.3.2)	P25809
NEPHGE 231	BTHIL	ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9)	P17764
NEPHGE 236	Unknown	MWt: 43,200; pI: 7.90; Mass spec FIG. 38	
NEPHGE 253	Unknown	MWt: 39,100; pI: 9.05; Mass spec FIGs. 39-40	
NEPHGE 296	NC5R	NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2)	P20070
NEPHGE 306	KAD2	ADENYLATE KINASE ISOENZYME 2, MITOCHONDRIAL (EC 2.7.4.3)	P29410
NEPHGE 310	Unknown	MWt: 35,800; pI: 7.57; Mass spec FIG. 47	
NEPHGE 326	Unknown	MWt: 34,500; pI: 8.62; Mass spec FIG. 48	

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Gel Spot No.	Gene	Protein	Database Accession
NEPHGE 328	Unknown	MWt: 30,900; pI: 8.48	
NEPHGE 334	TPIS	TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM)	P48500

Example 8: Interleukin-1DF Induced Changes in the Protein Expression of Rat Islets: A Computerized Database

Summary

Two-dimensional (2-D) gel electrophoresis of pancreatic islet proteins can be an important tool facilitating studies of the molecular pathogenesis of insulin-dependent diabetes mellitus. Insulin-dependent diabetes mellitus is caused by an autoimmune destruction of the β-cells in the islets of Langerhans. The cytokine interleukin 1β inhibits insulin release and is selectively cytotoxic to β-cells in isolated pancreatic rat islets. The antigen(s) triggering the immune response as well as the intracellular mechanisms of action of interleukin 1β-mediated β-cell cytotoxicity are unknown. However, previous studies have found an association with alterations in protein synthesis. Thus, 2-D gel electrophoresis of islet proteins can lead to 1) the identification of primary antigen(s) initiating the immune destruction of the β-cells 2) the determination of qualitative and quantitative changes in specific islet proteins induced by cytokines and 3) the determination of the effects of agents modulating cytokine action. Therefore, the aim of this study was to create databases of all reproducibly detectable protein spots on 10% and 15% acrylamide 2-D gels of neonatal rat islets (10% & 15% DB), labelled under standardized culture conditions. 1792 spots were present in 5 of 5 gels in the 15% DB, whereas 1373 spots were present in 5 of 5 gels in the 10% DB, yielding a qualitative reproducibility between 75.2% and 91.7%. In both DBs, the average coefficient of variation of the percentage of integrated optical density (CV% of %IOD) for spots present in all gel was between 42.4% and 45.7%. When the same sample was analyzed in consecutive sets of gels on different days (interassay analysis), the average CV% of %IOD was 35.5%-36.1%. When the same sample was analyzed repeatedly in one set of gels (intraassay analysis), the average CV% of %IOD was 30.2% in the IEF gels, while the average CV% of %IOD was unchanged (45.7%) in the NEPHGE gels. Applying the 10% DB to distinguish proteins altered in expression by IL-1β, 105 currently unidentified protein spots were found to be up-/down-regulated or synthesized *de novo* by IL-1β. In conclusion, we present the first 10% and 15% acrylamide 2-D gel protein databases of neonatal rat islets of Langerhans and demonstrate its usage to identify proteins altered in expression by IL-1β.

Introduction

The cytokine interleukin 1β inhibits insulin release and is selectively cytotoxic to β-cells in isolated pancreatic rat islets (Mandrup-Poulsen, T, *Diabetologia, in press* (1996)). Active protein synthesis is a crucial part of β-cell destruction, defense and repair after insults such as cytokines. The free radical nitric oxide (NO) has been demonstrated

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to be an important mediator of the deleterious effects of cytokines on islet α-cells (Southern, *et al.*, *FEBS. Lett. 276*:42-44 (1990); Welsh, *et al.*, *Endocrinol. 129*:3167-3173 (1991); Corbett, *et al.*, *J. Biol. Chem. 266*:21351-21354 (1991)). Thus, analogues of L-arginine, the substrate for NO production, prevent the deleterious effects of interleukin 1β (IL-1β) (Southern, *et al.*, *FEBS. Lett. 276*:42-44 (1990); Welsh, *et al.*, *Endocrinol. 129*:3167-3173 (1991); Corbett, *et al.*, *J. Biol. Chem. 266*:21351-21354 (1991)) and mRNA for the cytokine-inducible isoform of NO synthase (iNOS) is induced by IL-1β in β-, but not α-cells (Corbett, *et al.*, *J. Clin. Invest. 90*:2384-2391 (1992)). We have recently cloned iNOS from neonatal rat islets and have demonstrated the expression of the recombinant iNOS as a series of spots on two-dimensional (2-D) gels, most likely as phosphorylated isoforms, with the expected molecular mass of 131 kDa and pI values in the range of 6.8 to 7.0 (Karlsen, *et al.*, *Diabetes 44*:753-758 (1995)).

Further, inhibitors of protein synthesis block the inhibitory effect of IL-1β on islet function (Hughes, *et al.*, *J. Clin. Invest. 86*:856-863 (1990)), indicating that *de novo* protein synthesis is necessary for the deleterious effect of IL-1β. IL-1β also induces the synthesis of the heat shock proteins (HSP) HSP32 (heme oxygenase) and HSP70 (Helqvist, *et al.*, *Acta Endocrinol. (Copenh.) 121*:136-140 (1989); Helqvist, *et al.*, *Diabetologia 34*:150-156 (1991); Welsh, *et al.*, *Autoimmunity 9*:33-40 (1991)), known to play a role in protection against cellular stress and in cell repair (Kaufmann, *Immunol. Today 11*:129-136 (1990)). Further, IL-1β inhibits the synthesis of a number of unknown proteins with molecular weights of 45, 50 (Hughes, *et al.*, *J. Clin. Invest. 86*:856-863 (1990)), 75, 85, 95 and 120 kDa (Welsh, *et al.*, *Autoimmunity 9*:33-40 (1991)) in islets. Using 2-D gel electrophoresis, we recently demonstrated that IL-1β up- and downregulated 29 and 3 proteins, respectively, in neonatal rat islets.

Endocrine islet cells can play an important role in β-cell destruction and, possibly, survival. Dispersion and sorting of islet cells is a potentially harmful procedure that could influence the protein synthesis pattern. The disadvantage of the chosen islet cell material is that any change in protein expression in one cell type will appear smaller because it is diluted by synthesis from other cells.

Thus, the aims of this study were to determine the spot detection reproducibility and to calculate the coefficient of variation of the percentage of integrated optical density (CV% of %IOD) for all (^{35}S)-methionine-labelled islet protein database spots. Additionally, we wanted to investigate the contribution of the intra- and interassay variation of the gel preparation to the total CV% of %IOD of the spots. Finally, we wanted to define the number of IL-1β-induced changes in the islet protein pattern by computer analysis.

Materials and Methods

Reagents. DMEM, RPMI 1640 and Hanks' balanced salt solution (HBSS) were purchased from Gibco, Paisley, Scotland. RPMI 1640 was supplemented with 20 mM HEPES buffer, 100,000 IU/l penicillin and 100 mg/L streptomycin. Authentic recombinant human IL-1β was provided by Novo Nordisk Ltd. (Bagsvaerd, Denmark). The specific activity was 400 U/ng (Moelvig, *et al., Scand. J. Immunol. 31*:225-235 (1990). The following other reagents were used: 2-mercaptoethanol, bovine serum albumin (BSA), Tris HCl, Tris base, glycine, (Sigma, St. Louis, USA); trichloracetic acid (TCA), phosphoric acid, NaOH, glycerol, n-butanol, bromophenol blue (Merck, Darmstadt, Germany); (^{35}S)-methionine (SJ 204, specific activity: >1.000 Ci/mmol, containing 0.1% 2-mercaptoethanol), Amplify® (Amersham International, Amersham, UK); filters (HAWP 0.25 μm pore size) (Millipore, Boston, USA); RNA'se A, DNA'se I (Worthington, Freehold, NJ, USA); urea (ultra pure) (Schwarz/Mann, Cambridge, MA, USA); acrylamide, bisacrylamide, TEMED, ammonium persulphate (BioRad, Richmond, CA, USA); ampholytes: pH 5-7, pH 3.5-10, pH 7-9, pH 8-9.5 (Pharmacia, Uppsala, Sweden); Nonidet P-40 (BDH, Poole, UK); ampholytes: pH 5-7 and sodium dodecyl sulphate (Serva, Heidelberg, Germany); agarose (Litex, Copenhagen, Denmark); ethanol (absolute 96%) (Danish Distillers, Aalborg, Denmark); methanol (Prolabo, Brione Le Blanc, France); acetic acid (technical quality, 99% glacial) (Bie & Berntsen, Århus, Denmark) and X-ray film (Curix RP-2) (AGFA).

Islet isolation and culture. For the database and assay variation experiments, 12 different islet isolations were performed, 10 for the databases, 1 for intraassay and 1 for interassay analysis. For the studies involving IL-1β, 3 additional islet isolations were performed.

Islets from pancreata of 4 day old inbred Wistar Furth rats (Møllegård, Lille Skensved, Denmark) were isolated after collagenase digestion (Brunstedt, *In:* Larner, J., Polh, S. L. (Eds.), *Methods In Diabetes Research, Vol. 1 (Laboratory methods, Part C).* Wiley & Sons, New York, pp. 254-288 (1984)). After a preculture period of 4 days in RPMI 1640 + 10% fetal calf serum, 150 islets were incubated for 24 h in 300 μl RPMI 1640 + 0.5% normal human serum (NHS). In a separate series of experiments, 150 islets were incubated for 24 h in 300 μl RPMI 1640 + 0.5% NHS with or without the addition of 150 pg/ml IL-1β.

Islet labelling. After 24 h in culture, the 150 islets were harvested, washed twice in HBSS and labelled for 4 h in 200 μl methionine-free Dulbecco's modified Eagle's's medium (DMEM) with 10% NHS dialysed for amino acids, and 200 μCi (^{35}S)-methionine. To eliminate 2-mercaptoethanol (^{35}S)-methionine was freeze-dried for at least 4 h before labelling. After labelling, islets were washed thrice in HBSS, pelleted and frozen at -80°C.

Sample preparation. The frozen islets were resuspended in 100 μl DNAse I/RNAse A solution and lysed by freeze-thawing twice. After the second thawing they

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were left on ice for 30 min for the digestion of nucleic acids. The lysed sample was then freeze dried overnight. The samples were dissolved by shaking in 120 µl lysis buffer (8.5 M urea, 2% Nonidet P-40, 5% 2-mercaptoethanol and 2% ampholytes pH range 7-9) for a minimum of 4 h.

Determination of (^{35}S)-methionine incorporation. The amount of (^{35}S)-methionine incorporation was quantitated in duplicate by adding 10 µg BSA (0.2 µg/ml H_2O) as a carrier to 5 µl of a 1:10 dilution of each sample, followed by 0.5 ml of 10% TCA. This was left to precipitate for 30 min at 40°C before being filtered through 0.25 µm filters. The HAWP filters were dried and placed into scintillation liquid for counting.

2-D gel electrophoresis. The procedure was essentially as described by O'Farrell *et al., Cell 12:*1133-1142 (1977) and Fey, S.J. *et al., The protein variation in basal cells and certain basal cell related benign and malignant diseases,* Faculty of Natural Science, University of Aarhus, Denmark (1984). Briefly, first dimension gels contained 4% acrylamide, 0.25% bisacrylamide and ampholytes (the actual ratio depending upon the batch) and were 175 mm long and 1.55 mm in diameter. Equal numbers of counts (10^6 cpm) of each sample were applied to the gels. In case of lower amounts of radioactivity it was necessary to regulate the exposure time of the gel so that comparable total optical densities were obtained. The samples were analyzed on both isoelectric focusing (IEF; pH 3.5-7) and non-equilibrium pH-gradient electrophoresis (NEPHGE; pH 6.5-10.5) gels. IEF gels were prefocused for approximately 4 h at 140 µA/gel (limiting current), the sample was then applied and focused for 18 h at 1200 V (limiting voltage). NEPHGE gels were focused for approximately 6.5 h using 140 µA/gel and 1200 V as the limiting parameters.

Second dimension gels, 1 mm thick, 200 mm long and 185 mm wide contained either 15% acrylamide and 0.075% bisacrylamide or 10% acrylamide and 0.05% bisacrylamide and were run overnight. After electrophoresis, the gels were fixed in 45% methanol and 7.5% acetic acid for 45 min and treated for fluorography with Amplify® for 45 min before being dried. The gels were placed in contact with X-ray films and exposed at -70°C for 1 to 40 days. Each gel was exposed for at least 3 time periods to compensate for the lack of dynamic range of X-ray films.

Determination of MW and pI. Molecular weights of the proteins were determined by comparison with standard gels (Fey, S.J. *et al., The protein variation in basal cells and certain basal cell related benign and malignant diseases,* Faculty of Natural Science, University of Aarhus, Denmark (1984)). pI for the individual proteins on the gels was determined by the use of pI calibration kits. Landmark proteins were identified on gels by one or several of the following techniques: immunoblotting, immunoprecipitation, microsequencing or peptide mapping.

Experimental design. The study comprised three different series of analyses: database, intra- and interassay analysis. For each analysis, IEF and NEPHGE gels were run using 10% and 15% acrylamide in the second dimension. This gave us four subgroups:

10% IEF; 15% IEF; 10% NEPHGE; 15% NEPHGE. On 10% acrylamide gels, the approximate MW range of detection were between 20 and 250 kDa, while the approximate range of detection was between 6 and 125 kDa on 15% acrylamide gels. Consequently, proteins with a MW between 20 and 125 kDa were included in both databases, whereas proteins with lower and higher MW were particular to 15% and 10% DBs, respectively. Comparison of 10% and 15% DBs revealed a lower number of detectable spots in both 10% IEF and NEPHGE subgroups (see Results). Consequently, intra- and interassay analysis (see below) were only performed on 15% IEF and NEPHGE gels.

The databases were based on 10 different isolates analyzed in one set of gels. After 2-D gel electrophoresis, 5 gels with the best technical quality and with comparable optical densities were chosen for computer analysis. Before computer analysis, one gel in each subgroup was arbitrarily selected to be the "master gel" used for comparison with the other 4 database gels, the 5 intraassay gels and the 5 interassay gels. The database "master gel" was used as a master for intra- and interassay analysis to ensure that a given spot had the same match number in the three series of analyses. Data from the "master gel" are only included in the database analysis. The "master gel" was from the same isolate in all 4 subgroups, whereas the identity of the isolates producing the 4 other database gels varied slightly from subgroup to subgroup (Table 3).

For intraassay analysis, 10 gels of the same sample were analyzed in one set of gels. After 2-D gel electrophoresis, 5 gels with the best technical quality and with comparable optical densities were chosen for computer analysis (Table 3).

For interassay analysis, the same sample was analyzed in 10 consecutive sets of gels on different days. After 2-D gel electrophoresis, 5 gels with the best technical quality and with comparable optical densities were chosen for computer analysis (Table 3).

For identification of proteins altered in expression by IL-1β, 10% IEF and NEPHGE gels of IL-1β exposed islets, previously analyzed visually (Andersen, *et al.*, *Diabetes 44*:400-407 (1995)), were matched to the 10% IEF and NEPHGE DBs.

Computer analysis of fluorographs. Computer analysis was performed using the BioImage® program (version 4.6 M) on a Sunsparc workstation. First, the fluorographs were scanned and spots were identified and quantitated by the BioImage® program BioImage, Ann Arbor, MA, USA. Next, each non-master gel was compared to the "master gel" and manually edited to ensure identification and quantitation of spots not found initially by the computer program. This comparison was performed by the same observer (H.U.A.) using the BioImage® program. Following this, the gels were matched by the BioImage® program and the accuracy of the match inspected and corrected by the same observer. Finally, data were extracted for calculations in the Quattro Pro® spreadsheet (Borland version 4.0).

To avoid the presence of duplicate spots in the IEF and NEPHGE subgroups, overlapping spots in either the basic part of IEF gels or in the acidic part of NEPHGE gels were omitted from analysis in the databases and the assay analyses.

Statistical analysis. Two different analyses were applied to distinguish the proteins altered in expression by IL-1β. In the first analysis, an alteration was considered significant if the average %IOD of a spot in IL-1β-exposed gels was higher or lower than the average %IOD ± 2 SD of the same spot in the DB. In the second comparison between the two groups, Student's t test was applied and $P < 0.01$ was chosen as level of significance.

Qualitative reproducibility of the neonatal rat islet protein databases and assay analyses. 1293 to 1411 (IEF) and 605 to 764 (NEPHGE) spots were found in the individual gels used to construct the 15% DB, whereas 1101 to 1200 (IEF) and 462 to 577 (NEPHGE) spots were found in the gels used for the 10% DB (Tables 4 and 5). "Master gels" were made for the 10% IEF and NEPHGE DB. In total, 1792 spots were present in 5 of 5 gels in the 15% DB, whereas 1373 spots were present in 5 of 5 gels in the 10% DB, yielding a qualitative reproducibility (the average of the percentage of spots found in 5 of 5 gels) in the subgroups between 75.2% (NEPHGE 10%) and 91.7% (IEF 15%) (Tables 4 and 5) (For each spot present in 5 of 5 gels, the databases consist of spot match number, %IOD for the 5 individual spots, average %IOD, standard deviation of %IOD, CV% of %IOD, MW and pI.).

As demonstrated in Tables 4 and 5, the total number of spots in the individual gels as well as the number and percentage of spots present in 5 of 5 gels were fewer in the 10% DB than in the 15% DB. However, if the databases were extended to include spots present in at least 3 of 5 gels, no differences in the percentage of spots present were found between the two databases (IEF: 15%: 98.8 ± 1.2; 10%: 97.4 ± 1.5; NEPHGE: 15%: 94.8 ±5.7; 10%: 94.1 ± 3.5, Tables 4 and 5). In both databases, the percentage of spots present in 5, 4, 3 or 2 of 5 gels were lower in NEPHGE gels than in IEF gels (Tables 4 and 5). The spatial location of the spots present in less than 5 gels was investigated, demonstrating that the spots were not grouped in specific areas of the gels depending on whether the spot was present in 1, 2, 3 or 4 gels.

Intra- and interassay analyses were only performed on 15% gels, since the number of detectable spots was higher in this database. In both analyses, the number of spots in the individual gels as well as the number and percentage of spots present in 5 of 5 gels were slightly (9%-19%) reduced compared to the 15% DB (compare Tables 4 and 6).

Quantitative reproducibility of the neonatal rat islet protein databases and assay analyses. The quantitative reproducibility was defined as the average of the CV% of %IOD for each spot present in 5 of 5 gels. For the databases, the average CV% was at a comparable level (42.4%-45.7%) in both 10% and 15% IEF and NEPHGE subgroups of gels (Table 7). For all DB subgroups the CV% ranged between 3.0% and 167.9% (Table 7). For interassay analyses, the average CV% were 35.5%-36.1% for both IEF and

NEPHGE gels, whereas the average CV% was 30.2% for the intraassay analysis of IEF gels and 45.7% for NEPHGE gels.

Subsequently, the database spots present in all gels were ranked in increasing order of CV% of %IOD, resulting in similar sigmoid-shaped curves for spots in all four database subgroups. Thus, 30% of the spots had a CV% that was lower than 29.7% -32.5%, 50% of the spots had a CV% that was lower than 37.8% - 42.8 %, 90% of the spots had a CV% that was lower than 68.4% - 80.6%. The slopes of the curves indicate that the 5%-10% spots with the highest CV% contribute significantly to the average CV% of %IOD. This is supported by the fact that the median values of the database subgroups are 2.3% to 5.5% lower than the mean values of the subgroups (Table 7).

Regression analyses between the average %IOD and CV% of %IOD for each spot in the database subgroups. In the NEPHGE 10% and 15% DB subgroups, 2 and 6, respectively, of the 10 spots with the highest average IOD% were found in the percentile with the lowest CV% (see above). Although none of the 10 spots with the highest average IOD% were found in this percentile in the IEF DB subgroups, regression analyses were performed to investigate whether a correlation existed between spot average %IOD and CV%. Regression analyses demonstrated that a significant negative correlation existed between these two parameters (range: $p=O$ (IEF 10%) - $p=0.00288$ (IEF 15%)). However, since the R^2-values were very low for all subgroups (range: $R^2=0.0072$ (IEF 15%) $R^2=0.0317$ (IEF 10%)), the majority of the variability-of CV% is not explained by variation in average %IOD.

Application of the 10% IEF and NEPHGE DB to distinguish proteins altered in expression by IL-1β. In a recent paper, we demonstrated that IL-1βB up and downregulated 29 and 4 proteins, respectively in 2-D gels of neonatal rat islet proteins (Andersen, *et al., Diabetes 44*:400-407 (1991)). 10% gels were prepared from (35S)-methionine labelled Wistar Furth neonatal rat islets cultured under similar conditions as the present study. Consequently, the rat islet 10% IEF and NEPHGE DB was used for comparison with the computer analyzed gels of IL-1β-exposed islets, analyzed visually in the previous paper (Andersen, *et al., Diabetes 44*:400-407 (1991)). Using ± 2 SD of IOD% of each DB spot as a cutoff level (comparable to the criterion for significant up- or down regulation in the visual analysis), comparison with the 10% DB confirmed 32 of these alterations and as expected identified several new protein changes. Thus, a total of 183 spots were upregulated, 113 downregulated and 34 synthesized *de novo* by IL-1β (results not shown). When using $p<0.01$ as a cutoff level in a Student's t test, the final analysis showed that 52 spots were upregulated, 47 downregulated- and 6 synthesized *de novo* by IL-1β, 13 of these included in the 33 spots selected by visual analysis.

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Discussion:

In this study, we present a 10% and 15% acrylamide 2-D gel protein DB of neonatal rat islets of Langerhans, comprising the first protein databases of islets or insulin secreting cells in any species. 1792 spots were present in 5 of 5 gels in the 15% DB, whereas 1373 spots were present in 5 of 5 gels in the 10% DB, yielding a qualitative reproducibility between 75.2% and 91.7%. In both databases, the average CV% of %IOD was between 42.4% and 45.7%. Applying the 10% DB to distinguish proteins altered in expression by IL-1β, 105 currently unidentified protein spots were found to be up-/down-regulated or synthesized *de novo* by IL-1β.

Characteristics of neonatal Wistar Furth rat islets. To reduce variability, the inbred Wistar Furth strain of rats was chosen as an islet donor for our databases. This strain is the inbred variant of the outbred Wistar routinely used for islet experiments in our lab (Andersen, *et al., Diabetes 43*:770-777 (1994)). We have previously determined that the function of Wistar Furth neonatal rat islets cultured with or without IL-1β is comparable to that of Wistar neonatal rat islets (Andersen, *et al. Diabetes 44*:400-407 (1995); Andersen, *et al., Acta Endocrinol. 120*:92-98 (1989)) and have determined the effects of IL-1β on the 2-D gel protein pattern of Wistar Furth islets (Andersen, *et al. Diabetes 44*:400-407 (1995)). Since the present databases are based on neonatal, and not adult rat islets, we can not exclude that the protein pattern of adult islets will be different. However, adult and neonatal islets from outbred Wistar rats are equally sensitive to the deleterious effect of IL-1. (Mandrup-Poulsen, *et al., Diabetes 36*:641-647 (1987)).

Each litter of newborn rats used for islet isolation typically consists of 8-12 pups with a varying frequency of males and females. Since comparison of Coomassie Blue-stained gels of liver proteins from male and female outbred Wistar rats revealed quantitative differences in 7 of 250 analyzed spots and since six proteins were found exclusively in males and one protein exclusively in females (Steiner, *et al., Electrophoresis 16*:1969-1976 (1995)), it is likely that some of the proteins in our database are gender-specific or gender-regulated. Consequently, it is possible that the high variation of some of the spots in our databases could be reduced if we had chosen to construct separate databases of islets from male and female rats. However, the gels of liver proteins were performed on non-cultured cells which could mean that the sex-determined protein variability could be induced by circulating sex steroids and not an inherent trait of the liver cells *per se.* Circulating hormones are not likely to interfere in our protein pattern since I) we preculture our islets for 4 days before experiments and II) no differences in serum concentrations of sex steroids are found before puberty. Further, we have previously demonstrated that islets from male and female outbred Wistar rats are equally sensitive to the deleterious effect of IL-1 (Steiner, *et al., Electrophoresis 16*:1969-1976 (1995)).

Detection of islet proteins. Not all spots detected in our databases will represent different protein entities, since some spots can represent modifications (*e.g.* acetylation,

methylation, phosphorylation or carbamylation) of other proteins. However, the detected number of spots is an underestimation of the total number of islet proteins, since the protein database does not include proteins below the limit of sensitivity, proteins not containing methionine, proteins with a molecular weight below 6 kDa or above 250 kDa

5   or proteins with a pH below 3.5 or above 10.5. Further, about 40% of the spots with IODs above limits of detection have previously been estimated to be missed because they are obscured by other spots (Garrels, *J. Biol. Chem. 264*:5269-5282 (1989)). Finally, the 4h labelling period favours the labelling of proteins with high synthesis rates, whereas longer labelling periods could be required to produce databases where all proteins are in steady-

10 state.

Qualitative reproducibility. Previous reports of the qualitative reproducibility of 2-D gel protein databases are few and the results variable: In a mouse liver protein database of Coomassie Blue-stained 2-D gels, 826 spots were present in the master image and on the average 500 spots were matched in 85% of the other mouse liver patterns

15 (Giometti, *et al., Electrophoresis 13*:970-991 (1992)). In protein databases of (^{35}S)-methionine labelled mouse embryos over 80% of spots in each of the four gel images were automatically matched to the standard image (Shi, *et al., Molec. Reprod. Develop. 37*:34-47 (1994)). In our study, 1792 spots (75.2% - 91.7%) were present in 5 of 5 gels in the 15% DB, whereas the average percentage of spots present in 5 of 5 gels was 5-10% lower

20 in the 10% DB. This is presumably due to the fact that fewer proteins exist in the high molecular weight region only analyzable on the 10% gels than in the low molecular weight region only analyzable on the 15% gels. In all groups analyzed, the qualitative reproducibility of NEPHGE gels was lower than IEF gels. Since NEPHGE gels, contrary to EF gels, are non-equilibrium gels the risk that identical spots have a slightly different

25 horizontal location is increased. However, our manual editing have ascertained that this problem has been eliminated as much as possible.

Quantitative reproducibility. Regarding the quantitative reproducibility, comparisons with other studies are difficult, since the methods used for spot identification are not identical. Further, the spots included in calculations of CV% of %IOD in most of

30 the previously published databases are selected from the total number of matched spots according to varying criteria. In ten Coomassie Blue-stained gels of male and female Wistar rat liver proteins, 250 of more than 1,000 spots present in the "master gel" were selected according to good shape, size and resolution and the presence and good quality in previous experiments (Steiner, *et al., Electrophoresis 16*:1969-1976 (1995)). Using

35 these criteria, one third of the spots had a CV% below 20%, more than half had a CV% below 30% and three quarters had a CV% below 40% (Steiner, *et al., Electrophoresis 16*:1969-1976 (1995)). In (^{35}S)-methionine labelled protein databases consisting of 5 gels of compacted eight-cell (CEC) mouse embryos and 4 gels of blastocyst-stage (BS) mouse embryos, 1,674 and 1,653 spots, respectively, were matched in all gels (Shi, *et al., Molec.*

Reprod. Develop. 37:34-47 (1994)). Calculated on the basis of all matched spots, the percentage error (defined as SEMx100/average) of 74% (CEC) or 79% (BS) of these spots was below 50%, and 45% (CEC) or 47% (BS) of the spots had a percentage error below 30% (Shi, *et al., Molec. Reprod. Develop. 37*:34-47 (1994)). For comparison, conversion of SD's to SEM's (SEM= SD/$\sqrt{n}$) would give an average CV% of 20.3% in the islet IEF 15% DB, and 97.7% and 83.2% of the spots would have a percentage error below 50% and 30%, respectively.

Although the quantitative reproducibility of our study is comparable to or even better than the study in mouse embryos (Shi, *et al., Molec. Reprod. Develop. 37*:34-47 (1994)), the average CV% of %IOD in our databases are still relatively high. As previously mentioned, the heterogeneous cell population of islets and the different male/female ratio of the islet isolations could contribute to gel variability. Although we have attempted to use gels with comparable total optical densities (the largest difference within each subgroup was by a factor of 3.5 (gel DB10 vs. gel DB3, IEF 15% DB, Table 3)), the non-linear saturation of X-ray film will contribute to the size of the CV% for all database spots. The application of phosphoimaging, a technique not available in our laboratory when this study was initiated, would reduce the contribution of this phenomenon to the magnitude of the CV%. Finally, electronic noise and differences in spot boundary definition in the computer analysis can contribute to the magnitude of the CV%. Contrary to some other gel analysis programs, the BioImage® program uses the local, and not the total background for boundary definition, reducing the contribution of the latter factor to the CV%.

Studies of replicate gels. In a study of 10 replicate gels of (^{35}S)-methionine labeled REF 52 cells, Garrels selected 1109 of the most prominent spots out of a total of approximately 2,000 spots and found an average CV% of 26.5%, with a range between <5% and > 100% and a modal value between 10% and 15% (Garrels, *J. Biol. Chem. 264*:5269-5282 (1989)). It is unclear whether the samples were analyzed in consecutive or the same set of gels. When grouping the spots according to spot quality (fitting to Gaussian shapes, overlapping of neighboring spots) and omitting spots with low density in all gels, the 19.1% spots of the highest quality had an average CV% of 13.0% (Garrels, *J. Biol. Chem. 264*:5269-5282 (1989)). As expected, the average CV% of %IOD was reduced when the 15% IEF and NEPHGE interassay analyses were compared to the 15% IEF DB, the reduction being by approximately 9%. Since the day-to-day variation of gel preparation was eliminated in the intraassay analyses, the average CV% was expected to decrease even more. In the 15% IEF subgroup, CV% was decreased by ≈15% compared to the database, whereas no decrease was found in the 15% NEPHGE subgroup. The reason for the high average CV% in the 15% NEPHGE intraassay subgroup, which also has the lowest qualitative reproducibility of all subgroups (Tables 4-6), is unknown. As the database gels were also analyzed in one set of gels, the fraction of the CV% that is

attributable to biological variation should be given by the difference in CV% between database and intraassay analysis for a given spot. Thus, if the result of the 15% NEPHGE intraassay analysis is disregarded, approximately one third of the average CV% of %IOD is due to biological variation.

5   *Effects of IL-1β on islet protein expression.* IL-1β altered the expression of 105 so far unidentified proteins. IL-1β mechanism of action on islet cells is not fully clarified, but three distinct groups of proteins might play important roles: proteins participating in signal-transduction and proteins encoded by so-called early response and late response genes (Eizirik, *et al., Diabetologia 39*:875-890 (1996)). IL-1β-induced signal transduction in
10   target cells is thought to involve four major signalling pathways: nuclear factor-κb, the stress-activated protein kinases (SAPK/JNK), protein kinase C and tyrosine kinase (Mandrup-Poulsen, T., *Diabetologia 39*:1005-1029 (1996); Eizirik, *et al., Diabetologia 39*:875-890 (1996)). The three pathways lead to a rapid and transient induction of the early response genes of which c-fos, c-jun and interferon response factor-1 have been implicated
15   in cytokine action on islet cells. The early response genes activate specific genes with possible deleterious (iNOS, cycloxygenase-2 and lipoxygenase) and protective (HSP72, haem oxygenase, Mn superoxide dismustase) action on islets (Mandrup-Poulsen, T., *Diabetologia, 39:*1005-1029 (1996); Eizirik, *et al., Diabetologia 39*:875-890 (1996)). Thus, the information about IL-1β mechanism of action in islet cells is still limited and the
20   identification of the 105 proteins altered in expression by IL-1β might lead to new knowledge about signal transduction and proteins with protective and deleterious actions.
Conclusion

We have established a protein database of neonatal rat islets of Langerhans with a high qualitative reproducibility and a quantitative reproducibility that improves on
25   previously published databases on other cells and tissues. Further, we have determined intra- and interassay variations of the neonatal rat islet protein database. The database has further been applied to identify proteins altered in expression by IL-1β, which might have important roles in an IL-1β mechanism of action. Since IL-1β is cytotoxic to the insulin producing rat B cells, identification of these proteins, currently being performed by mass
30   spectrometry and microsequencing, is expected to result in significant knowledge about the pathogenesis of insulin dependent diabetes mellitus.

Table 3. Correcti n fact rs between the t tal ptical densities f master and non-master gels in DB, intra- and interassay analyses of 2-D gels of neonatal rat islet proteins.					
15% gels					
		IEF			
DB		Interassa y		Intraassa y	
gel DB10 (master):	1	gel IE3:	1	gel IA2:	1
gel DB3:	0.293	gel IE4:	1.096	gel IA3:	0.620
gel DB6:	0.303	gel IE8:	1.129	gel IA4:	0.738
gel DB8:	0.840	gel IE9:	0.784	gel IA6:	1.014
gel DB9:	0.284	gel IE10:	0.804	gel IA10:	0.747
		NEPHGE			
DB		Interassa y		Intraassa y	
gel DB10 (master):	1	gel IE3:	1	gel IA1:	1
gel DB3:	0.542	gel IE4:	1.901	gel IA2:	1.599
gel DB6:	1.067	gel IE8:	1.761	gel IA3:	0.841
gel DB8:	0.986	gel IE9:	1.408	gel IA4:	0.908
gel DB9:	0.831	gel IE10:	1.599	gel IA5:	1.135
10% gels					
IEF		NEPHGE			
DB		DB			
gel DB10 (master):	1	gel DB10 (master):		1	
gel DB1:	0.947	gel DB1:		1.660	
gel DB4:	0.358	gel DB7:		3.215	
gel DB6:	1.167	gel DB8:		2.959	
gel DB8:	1.145	gel DB9:		1.197	

The databases were based on 10 different isolates analyzed in one set of gels, while interassay analysis consisted of 10 gels of the same sample analyzed in one set of gels and interassay analysis was based on the analysis of the same sample run in 10 consecutive sets of gels on different days. Before computer analysis, one gel in each database subgroup was arbitrarily selected to be the "master gel" used for comparison with the other 4 database gels, the 5 intraassay gels and the 5 interassay gels. The numbers (1-10) of the isolates/replicates chosen are indicated in the Table. The correction factors between the total optical densities of the master and non-master gels were calculated in the BioImage® program following analysis. Gels with a correction factor <1 have a higher total optical density than the "master gel", e.g., in the 15% IEF DB, the total optical density of gel DB10 = 0.293 x gel DB3. For the intra- and interassay analyses, correction factors were calculated between an arbitrarily selected gel and the 4 other gels. Comparison cannot be made between subgroups because gels with a correction factor of 1 not necessarily have the same intensity.

Table 4. Reproducibility of spot detection in 15% IEF and NEPHGE 2-DGE DB of neonatal rat islet proteins.

IEF	total no. of spots	spots in 5 of 5 gels		spots in 4-5 of 5 gels		spots in 3-5 of 5 gels		spots in 2-5 of 5 gels	
		no.	%	no.	%	no.	%	no.	%
gel DB3	1325	1235	93.2	1299	98.0	1320	99.6	1325	100
gel DB6	1352	1235	91.3	1322	97.8	1346	99.6	1352	100
gel DB8	1293	1235	95.5	1276	98.7	1287	99.5	1292	99.9
gel DB9	1355	1235	91.1	1319	97.3	1339	98.8	1355	100
gel DB10	1411	1235	87.5	1327	94.0	1365	96.7	1398	99.1
avg ± SD			91.7 ± 3.0		97.2 ± 1.8		98.8 ± 1.2		99.8 ± 0.4
NEPHGE									
gel DB3	663	557	84.0	604	91.1	633	95.5	658	99.2
gel DB6	605	557	92.1	584	96.5	598	98.8	604	99.8
gel DB8	629	557	88.6	597	94.9	614	97.6	623	99.0
gel DB9	634	557	87.9	601	94.8	617	97.3	630	99.4
gel DB10	764	557	72.9	610	79.8	648	84.4	701	91.8
avg ± SD			85.1 ± 7.4		91.4 ± 6.8		94.8 ± 5.7		97.8 ± 3.4

Construction of the 2-D gel gel database: neonatal rat islets from 5 different isolates were cultured for 24 h in RPMI 1640 + 0.5% HS, washed twice and labelled for 4h with (^{35}S)-methionine. Following 2-DGE (see Materials and Methods) in one set of gels, the fluorographs were scanned and spots were identified and quantitated by the BioImage® program. Each gel was compared and matched to the arbitrarily selected "master gel" (gel DB10). For each gel, the table indicates the number and percentage of spots present in (from left to right) all gels, at least 4 of 5 gels, at least 3 of 5 gels and at least 2 of 5 gels.

Table 5. Reproducibility of spot detection in 10% IEF and NEPHGE 2-DGE DB of neonatal rat islet proteins.

IEF	total no. of spots	spots in 5 of 5 gels		spots in 4-5 of 5 gels		spots in 3-5 of 5 gels		spots in 2-5 of 5 gels	
		no.	%	no.	%	no.	%	no.	%
gel DB1	1101	995	90.4	1060	96.3	1070	97.2	1072	97.4
gel DB4	1200	995	82.9	1094	91.2	1143	95.3	1163	96.9
gel DB6	1120	995	88.8	1075	96.0	1106	98.8	1108	98.9
gel DB8	1119	995	88.9	1084	96.9	1106	98.8	1113	99.5
gel DB10	1198	995	83.1	1106	92.3	1162	97.0	1193	99.6
avg ± SD			86.8 ± 3.5		94.5 ± 2.6		97.4 ± 1.5		98.5 ± 1.2
NEPHGE									
gel DB1	516	378	73.3	438	84.9	475	92.1	489	94.8
gel DB7	462	378	81.8	424	91.8	442	95.7	445	96.3
gel DB8	480	378	78.8	440	91.7	468	97.5	472	98.3
gel DB9	492	378	76.8	441	89.6	474	96.3	482	98.0
gel DB10	577	378	65.5	455	78.9	513	88.9	539	93.4
avg ± SD			75.2 ± 6.3		87.4 ± 5.5		94.1 ± 3.5		96.2 ± 2.1

Construction of the 2-D gel database: neonatal rat islets from 5 different isolates were cultured for 24 h in RPMI 1640 + 0.5% HS, washed twice and labelled for 4h with (^{35}S)-methionine. Following 2-DGE (see Materials and Methods) in one set of gels, the fluorographs were scanned and spots were identified and quantitated by the BioImage® program. Each gel was compared and matched to the arbitrarily selected "master gel" (gel DB10). For each gel, the table indicates the number and percentage of spots present in (from left to right) all gels, at least 4 of 5 gels, at least 3 of 5 gels and at least 2 of 5 gels.

Table 6. Reproducibility of spot detection in replicate 15% IEF and NEPHGE 2-D gels of neonatal rat islet proteins.

Intraassay analysis					Interassay analysis				
	IEF	total no. of spots	spots in 5 of 5 gels			IEF	total no. of spots	spots in 5 of 5 gels	
			no.	%				no.	%
	gel IA2	1289	1085	84.2		gel IE3	1319	1082	82.0
	gel IA3	1337	1085	81.2		gel IE4	1348	1082	80.3
	gel IA4	1289	1085	84.2		gel IE8	1333	1082	81.2
	gel IA6	1303	1085	83.3		gel IE9	1342	1082	83.2
	gel IA10	1326	1085	81.8		gel IE10	1300	1082	80.6
	avg ± SD			82.9 ± 1.4		avg ± SD			81.5 ± 1.2
NEPHGE									
	gel IA1	526	345	65.6		gel IE3	574	421	75.0
	gel IA2	542	345	63.7		gel IE4	589	421	73.3
	gel IA3	538	345	64.1		gel IE8	566	421	71.5
	gel IA4	565	345	61.1		gel IE9	590	421	74.4
	gel IA5	450	345	76.7		gel IE10	561	421	71.4
	avg ± SD			66.2 ± 6.1		avg ± SD			73.1 ± 1.6

For intraassay analysis, 5 independent gels of the same islet cell lysate were analyzed in one set of gels. For interassay analysis, 5 independent gels of the same islet cell lysate were analyzed in consecutive sets of gels on different days. Different islet isolates were used for database, intra- and interassay analysis. When analyzed in the BioImage® program, the fluorographs were compared and matched to the 15% IEF of the NEPHGE "master gel" of Table 2.

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Table 7. Average coefficients of variance of % integrated optical density of spots detectable in 5 of 5 gels in databases and replicate 2-D gels of neonatal rat islet proteins.		
Analysis	Average CV%	Median (Range) CV%
IEF 15% DB	45.4 ± 25.0	39.9 (5.0-165.3)
IEF 15% Interassay	36.1 ± 19.8	32.6 (2.7-190.6)
IEF 15% Intraassay	30.2 ± 17.1	27.3 (0.0-130.4)
NEPHGE 15% DB	44.3 ± 22.5	42.0 (3.9-155.1)
NEPHGE 15% Interassay	35.5 ± 19.7	33.1 (2.2-118.5)
NEPHGE 15% Intraassay	45.7 ± 22.8	43.9 (4.3-130.9)
IEF 10% DB	45.7 ± 21.3	42.7 (3.0-133.4)
NEPHGE 10% DB	42.4 ± 22.4	37.7 (7.3-167.9)

The average coefficient of variance (CV%) was calculated from the CV% of %IOD of all spots present in 5 of 5 gels in each subgroup of analysis. Results are presented as means ± SD (left column) and as medians (ranges). The number of spots in 5 of 5 gels in each subgroup is shown in Tables 2-4. For details of design databases and replicate analyses, please see Materials and Methods.

Table 8. Proteins Present in Unaffected or Normal Rat Islet Cells

IEF 10% gels				NEPHGE 10% gels			
match no.	%IOD ratio	mw	pI	match no.	%IOD ratio	mw	pI
11	2.34	118,652	6.64	7	0.38	65,522	7.28
15	0.29	75,443	6.01				
25	1.79	54,244	5.53	17	5.09	39,973	8.29
28	2.65	65,798	5.06				
83	2.56	164,145	6.34	102	0.45	63,560	7.26
85	4.21	164,145	6.28				
115	2.56	175,154	5.23	129	0.32	57,609	7.72
145	8.51	133,052	6.29	130	0.45	55,734	8.07
				156	3.22	55,550	8.71
186	22.00	152,077	5.01	169	2.16	55,642	8.23
187	6.19	152,077	4.95	171	0.21	52,860	8.20
189	1.88	135,100	4.96	174	0.43	53,830	7.92
194	3.31	139,291	4.65	176	0.21	52,598	7.96
201	2.48	143,611	4.10	181	0.20	49,422	7.40
210	3.19	114,519	6.40	182	0.55	54,098	7.61
				203	1.51	44,362	8.19
225	4.06	83,281	5.89	211	0.28	47,925	7.28
265	3.31	120,019	4.99	227	0.29	43,939	8.43
267	2.12	92,500	4.78	231	0.41	44,362	8.34
276	2.52	107,498	4.34	236	0.16	43,162	7.90
279	6.78	121,401	4.20	253	0.25	39,106	9.05
				269	9.04	39,863	8.01
289	1.95	73,880	6.44	296	2.96	36,169	8.29
306	2.65	75,706	6.20	298	0.07	36,382	8.32
310	1.88	69,383	5.70	306	0.09	35,666	8.14
329	2.23	72,856	5.27	310	0.27	35,827	7.57
330	2.74	68,809	5.35	326	0.17	34,521	8.62
				328	0.03	30,920	8.48
				334	0.11	30,920	8.17
342	2.80	83,281	4.81				
354	6.23	70,358	4.30				
358	0.19	76,975	4.11				
382	2.55	63,920	6.35				
387	2.41	64,342	6.14				
425	2.09	67,198	5.18				
436	0.38	66,407	4.76				
441	0.22	66,758	4.62				
442	0.16	66,934	4.53				
471	2.81	60,722	6.08				
483	1.72	61,204	5.71				
484	0.27	59,247	5.88				
505	2.30	61,526	5.41				
506	2.34	60,007	5.42				
507	2.72	59,928	5.33				
510	0.26	54,485	5.27				
561	2.52	49,312	6.00				
563	3.04	48,018	6.20				
655	1.85	41,355	6.15				
665	0.33	42,243	5.82				
719	0.69	39,558	6.55				
759	2.40	37,116	5.34				
825	0.13	35,027	5.10				
831	0.53	34,623	4.76				
882	0.10	30,920	4.94				
887	0.24	30,837	4.76				
895	0.69	28,893	4.29				
908	0.27	25,753	6.28				

939	0.37	25,851	5.09
941	0.08	22,704	5.15
949	0.21	26,803	4.49
1,081	2.68	63,836	5.43
1,342	3.74	53,379	4.64

The match numbers of the table correspond to the match numbers of the 1 0% IEF and NEPHGE DBs. The spot numbers given in a previous paper (i 2) to spots altered in expression by IL-1 B are indicated in parenthesis. * indicates that the spot was not previously found to be altered in expression by IL-1 B alone but by other experimental conditions (1 2). For I EF and N EPHG E gels, the analysis was based on 5 DB gels and 3 IL-LB gels and P < 0.01 was chosen as level of signfficance. The %IOD ratio expresses the average %IOD of IL-1 B gels/average %IOD of DB gels. Thus, a ratio above 1 indicates that the spot is upregulated. DN indicates that the spot is synthesized *de novo* by IL-1 B.

Table 9. Affected Proteins up-/down-regulated or synthesized de novo by IL-l B Treatment or Expected to be up-/down-regulated or synthesized de novo in Islet Cells when Immunologically Affected in IDDM.

IEF 10% gels				NEPHGE 10% gels			
match no.	%IOD ratio	mw	pI	match no.	%IOD ratio	mw	pI
				1	0.17	58,801	8.27
11	2.34	118,652	6.64	7	0.38	65,522	7.28
15	0.29	75,443	6.01				
25	1.79	54,244	5.53	17	5.09	39,973	8.29
28	2.65	65,798	5.06				
83	2.56	164,145	6.34	102	0.45	63,560	7.26
85	4.21	164,145	6.28				
115	2.56	175,154	5.23	129	0.32	57,609	7.72
145	8.51	133,052	6.29	130	0.45	55,734	8.07
				156	3.22	55,550	8.71
186	22.00	152,077	5.01	169	2.16	55,642	8.23
187	6.19	152,077	4.95	171	0.21	52,860	8.20
189	1.88	135,100	4.96	174	0.43	53,830	7.92
194	3.31	139,291	4.65	176	0.21	52,598	7.96
201	2.48	143,611	4.10	181	0.20	49,422	7.40
210	3.19	114,519	6.40	182	0.55	54,098	7.61
				203	1.51	44,362	8.19
225	4.06	83,281	5.89	211	0.28	47,925	7.28
265	3.31	120,019	4.99	227	0.29	43,939	8.43
267	2.12	92,500	4.78	231	0.41	44,362	8.34
276	2.52	107,498	4.34	236	0.16	43,162	7.90
279	6.78	121,401	4.20	253	0.25	39,106	9.05
				269	9.04	39,863	8.01
289	1.95	73,880	6.44	296	2.96	36,169	8.29
306	2.65	75,706	6.20	298	0.07	36,382	8.32
310	1.88	69,383	5.70	306	0.09	35,666	8.14
329	2.23	72,856	5.27	310	0.27	35,827	7.57
330	2.74	68,809	5.35	326	0.17	34,521	8.62
				328	0.03	30,920	8.48
				334	0.11	30,920	8.17
342	2.80	83,281	4.81				
				668	DN	42,809	8.46
354	6.23	70,358	4.30				
358	0.19	76,975	4.11				
382	2.55	63,920	6.35				
387	2.41	64,342	6.14				
425	2.09	67,198	5.18				
436	0.38	66,407	4.76				
441	0.22	66,758	4.62				
442	0.16	66,934	4.53				
471	2.81	60,722	6.08				
483	1.72	61,204	5.71				
484	0.27	59,247	5.88				
505	2.30	61,526	5.41				
506	2.34	60,007	5.42				
507	2.72	59,928	5.33				
510	0.26	54,485	5.27				
561	2.52	49,312	6.00				
563	3.04	48,018	6.20				
655	1.85	41,355	6.15				
665	0.33	42,243	5.82				
719	0.69	39,558	6.55				
759	2.40	37,116	5.34				

825	0.13	35,027	5.10
831	0.53	34,623	4.76
882	0.10	30,920	4.94
887	0.24	30,837	4.76
895	0.69	28,893	4.29
908	0.27	25,753	6.28
939	0.37	25,851	5.09
941	0.08	22,704	5.15
949	0.21	26,803	4.49
1,081	2.68	63,836	5.43
1,342	3.74	53,379	4.64
1,356	DN	147,898	5.40

The match numbers of the table correspond to the match numbers of the 10% IEF and NEPHGE DBs. The spot numbers given in a previous paper (i 2) to spots altered in expression by IL-1 B are indicated in parenthesis. * indicates that the spot was not previously found to be altered in expression by IL-1 B alone but by other experimental conditions (1 2). For IEF and N EPHG E gels, the analysis was based on 5 DB gels and 3 IL-LB gels and P < 0.01 was chosen as level of signfficance. The %IOD ratio expresses the average %IOD of IL-1 B gels/average %IOD of DB gels. Thus, a ratio above 1 indicates that the spot is upregulated. DN indicates that the spot is synthesized *de novo* by IL-1 B.

Table 10. Marker Proteins In Islet Cells

IEF 10% gels				NEPHGE 10% gels			
match no.	%IOD ratio	mw	pI	match no.	%IOD ratio	mw	pI
11	2.34	118,652	6.64	7	0.38	65,522	7.28
15	0.29	75,443	6.01				
25	1.79	54,244	5.53	17	5.09	39,973	8.29
28	2.65	65,798	5.06				
83	2.56	164,145	6.34	102	0.45	63,560	7.26
85	4.21	164,145	6.28				
115	2.56	175,154	5.23	129	0.32	57,609	7.72
145	8.51	133,052	6.29	130	0.45	55,734	8.07
				156	3.22	55,550	8.71
186	22.00	152,077	5.01	169	2.16	55,642	8.23
187	6.19	152,077	4.95	171	0.21	52,860	8.20
189	1.88	135,100	4.96	174	0.43	53,830	7.92
194	3.31	139,291	4.65	176	0.21	52,598	7.96
201	2.48	143,611	4.10	181	0.20	49,422	7.40
210	3.19	114,519	6.40	182	0.55	54,098	7.61
				203	1.51	44,362	8.19
225	4.06	83,281	5.89	211	0.28	47,925	7.28
265	3.31	120,019	4.99	227	0.29	43,939	8.43
267	2.12	92,500	4.78	231	0.41	44,362	8.34
276	2.52	107,498	4.34	236	0.16	43,162	7.90
279	6.78	121,401	4.20	253	0.25	39,106	9.05
				269	9.04	39,863	8.01
289	1.95	73,880	6.44	296	2.96	36,169	8.29
306	2.65	75,706	6.20	298	0.07	36,382	8.32
310	1.88	69,383	5.70	306	0.09	35,666	8.14
329	2.23	72,856	5.27	310	0.27	35,827	7.57
330	2.74	68,809	5.35	326	0.17	34,521	8.62
				328	0.03	30,920	8.48
				334	0.11	30,920	8.17
342	2.80	83,281	4.81				
354	6.23	70,358	4.30				
358	0.19	76,975	4.11				
382	2.55	63,920	6.35				
387	2.41	64,342	6.14				
425	2.09	67,198	5.18				
436	0.38	66,407	4.76				
441	0.22	66,758	4.62				
442	0.16	66,934	4.53				
471	2.81	60,722	6.08				
483	1.72	61,204	5.71				
484	0.27	59,247	5.88				
505	2.30	61,526	5.41				
506	2.34	60,007	5.42				
507	2.72	59,928	5.33				
510	0.26	54,485	5.27				
561	2.52	49,312	6.00				
563	3.04	48,018	6.20				
655	1.85	41,355	6.15				
665	0.33	42,243	5.82				
719	0.69	39,558	6.55				
759	2.40	37,116	5.34				
825	0.13	35,027	5.10				
831	0.53	34,623	4.76				
882	0.10	30,920	4.94				
887	0.24	30,837	4.76				
895	0.69	28,893	4.29				
908	0.27	25,753	6.28				

939	0.37	25,851	5.09
941	0.08	22,704	5.15
949	0.21	26,803	4.49
1,081	2.68	63,836	5.43
1,342	3.74	53,379	4.64

5

The match numbers of the table correspond to the match numbers of the 10% IEF and NEPHGE DBs. The spot numbers given in a previous paper (i 2) to spots aftered in expression by IL-1 B are indicated in parenthesis. * indicates that the spot was not previously found to be aftered in expression by IL-1 B alone but by other experimental conditions (1 2). For I EF and N EPHG E gels, the analysis was based on 5 DB gels and 3 IL-LB gels and P < 0.01 was chosen as level of signfficance. The %IOD ratio expresses the average %IOD of IL-1 B gels/average %IOD of DB gels. Thus, a ratio above 1 indicates that the spot is upregulated. DN indicates that the spot is synthesized *de novo* by IL-1 B.

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Table 11. Optional Proteins Present in Unaffected or Normal Islet Cells

	IEF 10% gels				NEPHGE 10% gels			
	match no.	%IOD ratio	mw	pI	match no.	%IOD ratio	mw	pI
5	10(7-)	11.57	120,478	7.27	9 (3)	0.12	115,709	8.33
					18 (18)	0.27	36,415	8.44
					123 (8)	0.29	57,040	8.17
	173(3)	2.47	136,657	5.38				
	217(8)	4.73	91,294	6.12				
10	285(10)	6.01	78,333	6.66				
	339(12)	0.16	72,602	5.12				
	340(13)	0.32	71,346	5.20				
	344(11-)	0.44	73,622	4.95				
	347(14)	4.05	77,651	4.62				
15	480(18)	4.20	62,014	5.91				
	614(21)	0.27	52,937	4.76				
	950(26)	0.19	25,753	4.53				
	1,196(2)	0.55	143,064	5.41	. . .			

20   The match numbers of the table correspond to the match numbers of the 1 0% IEF and NEPHGE DBs. The spot numbers given in a previous paper (i 2) to spots altered in expression by IL-1 B are indicated in parenthesis. * indicates that the spot was not previously found to be altered in expression by IL-1 B alone but by other experimental conditions (1 2). For IEF and N EPHG E gels, the analysis was based on 5 DB gels and 3 IL-LB gels and P < 0.01 was chosen as level of signfficance. The %IOD ratio expresses the average %IOD of IL-1 B gels/average %IOD of DB gels. Thus, a ratio above 1 indicates that the spot is upregulated. DN indicates that the spot is synthesized *de novo* by IL-1 B.

Table 12. Optionally Affected Proteins up-/down-regulated or synthesized de novo by IL-l B Treatment or Expected to be up-/down-regulated or synthesized de novo in Islet Cells when Immunologically Affected in IDDM

IEF 10% gels				NEPHGE 10% gels			
match no. %IOD ratio		mw	pI	match no. %IOD ratio		mw	pI
10(7-)	11.57	120,478	7.27	9 (3)	0.12	115,709	8.33
				18 (18)	0.27	36,415	8.44
				123 (8)	0.29	57,040	8.17
173(3)	2.47	136,657	5.38				
217(8)	4.73	91,294	6.12				
285(10)	6.01	78,333	6.66				
339(12)	0.16	72,602	5.12				
340(13)	0.32	71,346	5.20				
344(11-)	0.44	73,622	4.95				
347(14)	4.05	77,651	4.62	670 (1)	DN	148,745	8.10
				672 (2)	DN	132,543	8.52
				673 (2)	DN	132,204	8.46
				674 (2)	DN	132,543	8.42
480(18)	4.20	62,014	5.91				
614(21)	0.27	52,937	4.76				
950(26)	0.19	25,753	4.53				
1,196(2)	9.55	143,064	5.41				

The match numbers of the table correspond to the match numbers of the 1 0% IEF and NEPHGE DBs. The spot numbers given in a previous paper (i 2) to spots aftered in expression by IL-1 B are indicated in parenthesis. * indicates that the spot was not previously found to be aftered in expression by IL-1 B alone but by other experimental conditions (1 2). For I EF and N EPHG E gels, the analysis was based on 5 DB gels and 3 IL-LB gels and $P < 0.01$ was chosen as level of signfficance. The %IOD ratio expresses the average %IOD of IL-1 B gels/average %IOD of DB gels. Thus, a ratio above 1 indicates that the spot is upregulated. DN indicates that the spot is synthesized *de novo* by IL-1 B.

Table 13. Optional Marker Proteins in Islet Cells

IEF 10% gels					NEPHGE 10% gels			
match					match			
no.	%IOD ratio	mw	pI		no.	%IOD ratio	mw	pI
10(7-)	11.57	120,478	7.27		9 (3)	0.12	115,709	8.33
					18 (18)	0.27	36,415	8.44
					123 (8)	0.29	57,040	8.17
173(3)	2.47	136,657	5.38					
217(8)	4.73	91,294	6.12					
285(10)	6.01	78,333	6.66					
339(12)	0.16	72,602	5.12					
340(13)	0.32	71,346	5.20					
344(11-)	0.44	73,622	4.95					
347(14)	4.05	77,651	4.62					
480(18)	4.20	62,014	5.91					
614(21)	0.27	52,937	4.76					
950(26)	0.19	25,753	4.53					
1,196(2)	0.55	143,064	5.41					

The match numbers of the table correspond to the match numbers of the 1 0% IEF and NEPHGE DBs. The spot numbers given in a previous paper (i 2) to spots altered in expression by IL-1 B are indicated in parenthesis. * indicates that the spot was not previously found to be altered in expression by IL-1 B alone but by other experimental conditions (1 2). For I EF and N EPHG E gels, the analysis was based on 5 DB gels and 3 IL-LB gels and P < 0.01 was chosen as level of significance. The %IOD ratio expresses the average %IOD of IL-1 B gels/average %IOD of DB gels. Thus, a ratio above 1 indicates that the spot is upregulated. DN indicates that the spot is synthesized *de novo* by IL-1 B.

All references cited herein, including journal articles or abstracts, published or corresponding U.S. or foreign patent applications, issued U.S. or foreign patents, or any other references, are entirely incorporated by reference herein, including all data, tables, figures, and text presented in the cited references. Additionally, the entire contents of the references cited within the references cited herein are also entirely incorporated by reference.

Reference to known method steps, conventional methods steps, known methods or conventional methods is not in any way an admission that any aspect, description or embodiment of the present invention is disclosed, taught or suggested in the relevant art.

The foregoing description of the specific embodiments will so fully reveal the general nature of the invention that others can, by applying knowledge within the skill of the art (including the contents of the references cited herein), readily modify and/or adapt for various applications such specific embodiments, without undue experimentation, without departing from the general concept of the present invention. Therefore, such adaptations and modifications are intended to be within the meaning and range of equivalents of the disclosed embodiments, based on the teaching and guidance presented herein. It is to be understood that the phraseology or terminology herein is for the purpose of description and not of limitation, such that the terminology or phraseology of the present specification is to be interpreted by the skilled artisan in light of the teachings and guidance presented herein, in combination with the knowledge of one of ordinary skill in the art.

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SEQUENCE LISTING

(1)   GENERAL INFORMATION:

       (i)   APPLICANT: Nerup, Jørn
                           Karlsen, Allan E.
                           Mose-Larsen, Peter
                           Fey, Steven J.
                           Bjerre Christensen, Ulla
                           Pociot, Flemming
                           Andersen, Henrik U.

       (ii)   TITLE OF INVENTION: Diabetes-Mediating Proteins and Therapeutic
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       (iii) NUMBER OF SEQUENCES: 10

       (iv)   CORRESPONDENCE ADDRESS:
              (A)   ADDRESSEE:Jorge A. Goldstein, Sterne, Kessler, Goldstein and
                     Fox, P.L.L.C.
              (B)   STREET: 1100 New York Ave., N.W., Suite 600
              (C)   CITY: Washington
              (D)   STATE: D.C.
              (E)   COUNTRY: U.S.A.
              (F)   ZIP: 20005

       (v)   COMPUTER READABLE FORM:
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       (ix)   TELECOMMUNICATION INFORMATION:
              (A)   TELEPHONE: 202 371 2600
              (B)   TELEFAX: 202 371 2540
(2)   INFORMATION FOR SEQ ID NO:1:
       (i)   SEQUENCE CHARACTERISTICS:
              (A)   LENGTH: 611 amino acids
              (B)   TYPE: amino acid
              (C)   TOPOLOGY: linear
       (ii)   MOLECULE TYPE: protein
       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Ile Ser Ala Ser Arg Ala Ala Ala Arg Leu Val Gly Thr Ala
              5                   10                  15

Ala Ser Arg Ser Pro Ala Ala Ala Arg Pro Gln Asp Gly Trp Asn Gly
              20              25                  30

Leu Ser His Glu Ala Phe Arg Phe Val Ser Arg Asp Tyr Ala Ser Glu
          35              40              45

Ala Ile Lys Gly Ala Val Val Gly Ile Asp Leu Gly Thr Thr Asn Ser
      50              55              60

Cys Val Ala Val Met Glu Gly Lys Gln Ala Lys Val Leu Glu Asn Ala
65              70              75              80

Glu Gly Ala Arg Thr Thr Pro Ser Val Val Ala Phe Thr Ala Asp Gly
              85              90              95

Glu Arg Leu Val Met Pro Ala Lys Arg Gln Ala Val Thr Asn Pro Asn
          100             105             110

Asn Thr Phe Tyr Ala Thr Lys Arg Leu Ile Gly Arg Arg Tyr Asp Asp
          115             120             125

Pro Glu Val Gln Lys Asp Thr Lys Asn Val Pro Phe Lys Ile Val Arg
      130             135             140

Ala Ser Asn Gly Asp Ala Trp Val Glu Ala His Gly Lys Tyr Ser Pro
145             150             155             160

Ser Gln Ile Gly Ala Phe Val Leu Met Lys Met Lys Glu Thr Ala Glu
              165             170             175

Asn Tyr Leu Gly His Thr Ala Lys Asn Ala Val Ile Thr Val Pro Ala
          180             185             190

Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly Gln Ile
          195             200             205

Ser Gly Leu Asn Val Leu Val Ile Asn Glu Pro Thr Ala Ala Ala Leu
      210             215             220

Ala Tyr Gly Leu Asp Lys Ser Glu Asp Lys Val Ile Ala Val Tyr Asp
225             230             235             240

Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Ile Gln Lys Gly
              245             250             255

Val Phe Glu Val Lys Ser Thr Asn Gly Asp Thr Phe Leu Gly Gly Asp
          260             265             270

Phe Asp Gln Ala Leu Leu Arg His Ile Val Lys Glu Phe Lys Arg Glu
          275             280             285

Thr Gly Val Asp Leu Thr Lys Asp Asn Met Ala Leu Gln Arg Val Arg
      290             295             300

Glu Ala Ala Glu Lys Ala Lys Cys Glu Leu Ser Ser Ser Val Gln Thr
305             310             315             320

Asp Ile Asn Leu Pro Tyr Leu Thr Asp Ala Ser Gly Pro Lys His Leu
              325             330             335

Asn Met Lys Leu Thr Arg Ala Gln Phe Glu Gly Ile Val Thr Asp Leu
          340             345             350
```

Ile Lys Arg Thr Ile Ala Pro Cys Gln Lys Ala Met Gln Asp Ala Glu
        355   360   365

Val Ser Lys Ser Asp Ile Gly Glu Val Ile Leu Val Gly Gly Met Thr
        370   375   380

Arg Pro Lys Val Gln Gln Thr Val Gln Asp Leu Phe Gly Arg Ala Pro
385   390   395   400

Ser Lys Ala Val Asn Pro Glu Asp Ala Val Ala Ile Gly Ala Ala Ile
                405   410   415

Gln Gly Gly Val Leu Ala Gly Asp Val Thr Asp Val Leu Leu Leu Asp
            420   425   430

Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Pro Pro Ala Pro Arg Gly
        435   440   445

Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Val
    450   455   460

His Val Ser Ala Lys Asp Lys Gly Thr Gly Arg Glu Gln Gln Ile Val
465   470   475   480

Ile Gln Ser Ser Gly Gly Leu Ser Lys Asp Asp Ile Glu Asn Met Val
                485   490   495

Lys Asn Ala Lys Tyr Ala Glu Glu Asp Arg Arg Lys Lys Glu Arg Val
            500   505   510

Glu Ala Val Asn Met Ala Glu Gly Ile Ile His Asp Thr Glu Thr Lys
        515   520   525

Met Glu Glu Phe Lys Asp Gln Leu Pro Ala Asp Glu Cys Asn Lys Leu
        530   535   540

Lys Glu Glu Ile Ser Lys Val Arg Ala Leu Leu Ala Lys Asp Ser Glu
545   550   555   560

Thr Gly Glu Asn Ile Arg Gln Ala Ala Ser Ser Leu Gln Gln Ala Ser
                565   570   575

Leu Lys Leu Phe Glu Met Ala Tyr Lys Lys Met Ala Ser Glu Arg Glu
            580   585   590

Gly Ser Gly Ser Ser Gly Thr Gly Glu Gln Lys Glu Asp Gln Lys Glu
        595   600   605

Glu Lys Gln
610

(2)   INFORMATION FOR SEQ ID NO: 2:
      (i)   SEQUENCE CHARACTERISTICS:
             (A)   LENGTH: 611 amino acids
             (B)   TYPE: amino acid
             (D)   TOPOLOGY: linear
      (ii)   MOLECULE TYPE: protein
      (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ile Ser Ala Ser Arg Ala Ala Ala Arg Leu Val Gly Ala Ala
                5   10   15

Ala Ser Arg Gly Pro Thr Ala Ala Arg His Gln Asp Ser Trp Asn Gly
            20   25   30

Leu Ser His Glu Ala Phe Arg Leu Val Ser Arg Asp Tyr Ala Ser Glu
        35   40   45

```
Ala Ile Lys Gly Ala Val Val Gly Ile Asp Leu Gly Thr Thr Asn Ser
    50              55              60
Cys Val Ala Val Met Glu Gly Lys Gln Ala Lys Val Leu Glu Asn Ala
65              70              75              80
Glu Gly Ala Arg Thr Thr Pro Ser Val Val Ala Phe Thr Ala Asp Gly
                85              90              95
Glu Arg Leu Val Met Pro Ala Lys Arg Gln Ala Val Thr Asn Pro Asn
            100             105             110
Asn Thr Phe Tyr Ala Thr Lys Arg Leu Ile Gly Arg Arg Tyr Asp Asp
        115             120             125
Pro Glu Val Gln Lys Asp Ile Lys Asn Val Pro Phe Lys Ile Val Arg
    130             135             140
Ala Ser Asn Gly Asp Ala Trp Val Glu Ala His Gly Lys Tyr Ser Pro
145             150             155             160
Ser Gln Ile Gly Ala Phe Val Leu Met Lys Met Lys Glu Thr Ala Glu
            165             170             175
Asn Tyr Leu Gly His Thr Ala Lys Asn Ala Val Ile Thr Val Pro Ala
            180             185             190
Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly Gln Ile
        195             200             205
Ser Gly Leu Asn Val Leu Val Ile Asn Glu Pro Thr Ala Ala Ala Leu
    210             215             220
Ala Tyr Gly Leu Asp Lys Ser Glu Asp Lys Val Ile Ala Val Tyr Asp
225             230             235             240
Leu Gly Gly Gly Thr Phe Asp Ile Ser Ile Leu Glu Ile Gln Lys Gly
            245             250             255
Val Phe Glu Val Lys Ser Thr Asn Gly Asp Thr Phe Leu Gly Gly Asp
            260             265             270
Phe Asp Gln Ala Leu Leu Arg His Ile Val Lys Glu Phe Lys Arg Glu
        275             280             285
Thr Gly Val Asp Leu Thr Lys Asp Asn Met Ala Leu Gln Arg Val Arg
    290             295             300
Glu Ala Ala Glu Lys Ala Lys Cys Glu Leu Ser Ser Ser Val Gln Thr
305             310             315             320
Asp Ile Asn Leu Pro Tyr Leu Thr Asp Ser Ser Gly Pro Lys His Leu
            325             330             335
Asn Met Lys Leu Thr Arg Ala Gln Phe Glu Gly Ile Val Thr Asp Leu
        340             345             350
Ile Arg Arg Thr Ile Ala Pro Cys Gln Lys Ala Met Gln Asp Ala Glu
        355             360             365
Val Ser Lys Ser Asp Ile Gly Glu Val Ile Leu Val Gly Gly Met Thr
    370             375             380
Arg Pro Lys Val Gln Gln Thr Val Gln Asp Leu Phe Gly Arg Ala Pro
385             390             395             400
Ser Lys Ala Val Asn Pro Glu Asp Ala Val Ala Ile Gly Ala Ala Ile
            405             410             415
```

Gln Gly Gly Val Leu Ala Gly Asp Val Thr Asp Val Leu Leu Leu Asp
        420   425   430

Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Pro Pro Ala Pro Arg Gly
        435   440   445

Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Val
    450   455   460

His Val Ser Ala Lys Asp Lys Gly Thr Arg Arg Glu Gln Gln Ile Val
465   470   475   480

Ile Gln Ser Ser Gly Gly Leu Ser Lys Asp Asp Ile Glu Asn Met Val
                485   490   495

Lys Asn Ala Lys Tyr Ala Glu Glu Asp Arg Arg Lys Lys Glu Arg Val
            500   505   510

Glu Ala Val Asn Met Ala Glu Gly Ile Ile His Asp Thr Glu Thr Lys
        515   520   525

Met Glu Glu Phe Lys Asp Gln Leu Pro Ala Asp Glu Cys Asn Lys Leu
    530   535   540

Lys Glu Glu Ile Ser Lys Met Arg Glu Leu Leu Ala Lys Asp Ser Glu
545   550   555   560

Thr Gly Glu Asn Ile Arg Gln Ala Ala Ser Ser Leu Gln Gln Ala Ser
                565   570   575

Leu Lys Leu Phe Glu Met Ala Tyr Lys Lys Met Ala Ser Glu Arg Glu
            580   585   590

Gly Ser Gly Ser Ser Gly Thr Gly Glu Gln Lys Glu Asp Gln Lys Glu
        595   600   605

Glu Lys Gln
    610

(2)   INFORMATION FOR SEQ ID NO: 3:
       (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 253 amino acids
                (B)   TYPE: amino acid
                (D)   TOPOLOGY: linear
       (ii)   MOLECULE TYPE: protein
       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ala Asp Gly Phe Ser Leu Asn Asp Ala Leu Ala Gly Ser Gly Asn
            5   10   15

Pro Asn Pro Arg Gly Trp Pro Gly Ala Trp Gly Asn Gln Pro Gly Ala
            20   25   30

Gly Gly Tyr Pro Gly Ala Ser Tyr Pro Gly Ala Pro Gly Gln Ala Pro
        35   40   45

Pro Gly Gly Tyr Pro Gly Gln Ala Pro Pro Ser Ala Tyr Pro Gly Pro
    50   55   60

Thr Gly Pro Ser Ala Tyr Pro Gly Pro Thr Ala Pro Gly Ala Tyr Pro
65   70   75   80

Gly Pro Thr Ala Pro Gly Ala Phe Pro Gly Gln Pro Gly Gly Pro Gly
                85   90   95

Ala Tyr Pro Ser Pro Gly Ala Tyr Pro Ser Ala Pro Gly Ala Tyr Pro
            100   105   110

```
Ala Thr Gly Pro Phe Gly Ala Pro Thr Gly Pro Leu Thr Val Pro Tyr
        115             120             125

Asp Met Pro Leu Pro Gly Gly Val Met Pro Arg Met Leu Ile Thr Ile
    125             130             135

Ile Gly Thr Val Lys Pro Asn Ala Asn Ser Ile Thr Leu Phe Lys Lys
140             145             150             155

Gly Asn Asp Ile Ala Phe His Phe Asn Pro Arg Phe Asn Glu Asn Asn
            160             165             170

Arg Arg Val Ile Val Cys Asn Thr Lys Gln Asp Asn Asn Trp Gly Arg
            175             180             185

Glu Glu Arg Gln Ser Ala Phe Pro Phe Glu Ser Gly Lys Pro Phe Lys
        190             195             200

Ile Gln Val Leu Val Glu Asp His Phe Lys Val Ala Val Asn Asp Val
    205             210             215

His Leu Leu Gln Tyr Asn His Arg Met Lys Asn Leu Arg Glu Ile Ser
220             225             230             235

Gln Leu Gly Ile Ile Gly Asp Ile Thr Leu Thr Ser Ala Ser His Ala
            240             245             250

Met Ile
```

(2)   INFORMATION FOR SEQ ID NO:4:
        (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 246 amino acids
                (B)   TYPE: amino acid
                (D)   TOPOLOGY: linear
        (ii)   MOLECULE TYPE: protein
        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Ala Asp Asn Phe Ser Leu His Asp Ala Leu Ser Gly Ser Gly Asn
                5               10              15

Pro Asn Pro Gln Gly Trp Pro Gly Ala Trp Gly Asn Gln Pro Ala Gly
            20              25              30

Ala Gly Gly Tyr Pro Gly Ala Ser Tyr Pro Gly Tyr Pro Gly Gln Ala
        35              40              45

Pro Pro Gly Ala Tyr Pro Gly Gln Ala Pro Pro Gly Ala Tyr His Gly
    50              55              60

Ala Pro Gly Ala Tyr Pro Gly Ala Pro Ala Pro Gly Val Tyr Pro Gly
65              70              75              80

Pro Pro Ser Gly Pro Gly Ala Tyr Pro Ser Ser Gly Gln Pro Ser Ala
            85              90              95

Pro Gly Ala Tyr Ala Thr Gly Pro Tyr Gly Ala Pro Ala Gly Pro Leu
        100             105             110

Ile Val Pro Tyr Asn Leu Pro Leu Pro Gly Gly Val Val Pro Arg Met
    115             120             125

Leu Ile Thr Ile Leu Gly Thr Val Lys Pro Asn Ala Asn Arg Ile Ala
    130             135             140

Leu Asp Phe Gln Arg Gly Asn Asp Val Ala Phe His Phe Pro Arg Phe
145             150             155             160

Asn Glu Asn Asn Arg Arg Val Ile Val Cys Asn Thr Lys Leu Asp Asn
```

Asn Trp Gly Arg Glu Glu Arg Gln Ser Val Phe Pro Phe Glu Ser Gly
            180   185   190

Lys Pro Phe Lys Ile Gln Val Leu Val Glu Pro Asp His Phe Lys Val
        195   200   205

Ala Val Asn Asp Ala His Leu Gln Tyr Asn His Arg Val Lys Lys Leu
    210   215   220

Asn Glu Ile Ser Lys Leu Gly Ile Ser Gly Asp Ile Asp Leu Thr Ser
225   230   235   240

Ala Ser Tyr Thr Met Ile
                245

(2)   INFORMATION FOR SEQ ID NO:5:
            (A)   LENGTH: 12 amino acids
            (B)   TYPE: amino acid
            (D)   TOPOLOGY: linear
        (ii)   MOLECULE TYPE: protein
        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Gln Tyr Glu Glu Leu Ile Ala Asn Gly Asp Met
            5   10

(2)   INFORMATION FOR SEQ ID NO:6:
        (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 10 amino acids
            (B)   TYPE: amino acid
            (D)   TOPOLOGY: linear
        (ii)   MOLECULE TYPE: protein
        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Lys Pro Leu Val Tyr Asp Glu Gly Lys
            5   10

(2)   INFORMATION FOR SEQ ID NO:7:
        (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 9 amino acids
            (B)   TYPE: amino acid
            (D)   TOPOLOGY: linear
        (ii)   MOLECULE TYPE: protein
        (xi)   SEQUENCE DESCRIPTION SEQ ID NO:7:

Leu Leu Glu Xaa Thr Xaa Xaa Leu Xaa
            5

(2)   INFORMATION FOR SEQ ID NO:8:
        (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 8 amino acids
            (B)   TYPE: amino acid
            (D)   TOPOLOGY: linear
        (ii)   MOLECULE TYPE: protein
        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Ser Leu Asn Ser Xaa Glu Xaa
            5

(2)   INFORMATION FOR SEQ ID NO:9:
        (i)   SEQUENCE CHARACTERISTICS:
            (A)   LENGTH: 7 amino acids
            (B)   TYPE: amino acid
            (D)   TOPOLOGY: linear
        (ii)   MOLECULE TYPE: protein
        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Ile Glu Leu Xaa Glu Ile Xaa
                5
```

(2)   INFORMATION FOR SEQ ID NO:10:
        (i)   SEQUENCE CHARACTERISTICS:
                (A)   LENGTH: 14 amino acids
                (B)   TYPE: amino acid
                (D)   TOPOLOGY: linear
        (ii)   MOLECULE TYPE: protein
        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Pro Glu Ala Ile Lys Gly Ala Val Val Gly Ile Asp Leu Gly
                5                   10
```

What Is Claimed Is:

1.   1. An *in vivo* method for identifying a diabetes-mediating protein, comprising:

(a)   obtaining cells or tissue which secrete insulin or are capable of developing into insulin-secreting cells;

(b)   transplanting said cells or tissue into a host mammal, wherein said host mammal is at risk for development of diabetes;

(c)   removing said transplanted cells or tissue from said host mammals at a plurality of time periods between transplantation and development of diabetes;

(d)   analyzing the protein expression of said removed cells or tissue,

(e)   comparing the expression of said protein at one time period in the presence of diabetes development with the expression of said protein in the absence of diabetes development to identify a protein which exhibit an altered expression as a result of development of diabetes, wherein said protein is a diabetes-mediating protein.

2.   The method of claim 1, wherein said cell is a pancreatic islet cell or a β cell.

3.   The method of claim 1, wherein said host mammal is immunologically compatible with said transplanted cell.

4.   The method of claim 1, wherein said analysis of protein expression is by gel electrophoresis, immunoblotting, mass spectrometry, or chromatography.

5.   The method of claim 4, wherein said electrophoresis is two dimensional gel electrophoresis.

6.   An isolated diabetes-mediating protein identified through the process of claim 1.

7.   A diabetes-mediating protein, wherein said protein is characterized as exhibiting an altered expression during development of diabetes, relative to expression of the same protein in the absence of diabetes.

8.   The diabetes-mediating protein of claim 7, wherein said protein is selected from the group consisting of the proteins listed in Tables 1 and 2.

9.   The diabetes-mediating protein of claim 7, wherein said protein is selected from the group of proteins characterized as having the mass spectroscopic characteristics of a protein shown in FIGs. 6-48.

10.   The protein of claim 7, wherein said protein is a protective protein, characterized as a protein capable of:

      (a)   protecting against the development of diabetes in a subject
               at risk for the development of diabetes;

      (b)   delaying the onset of diabetes in a subject at risk for the
               development of diabetes;

5   or

      (c)   ameliorating the symptoms of diabetes in a subject at risk
               for development of

diabetes.

      11.   The protein of claim 7, wherein said protein is a deleterious

10   protein, characterized as a protein capable of:

      (a)   enhancing the development of diabetes;

      (b)   increasing the risk of a subject developing diabetes;

      (c)   reducing the time required for development of diabetes in
               a subject at risk for development of diabetes; or

15   (d)   increasing the severity of the symptoms of diabetes.

      12.   A method for predicting the development of diabetes, comprising:

      (a)   measuring the expression of one or more of a protein
               shown in Table 1 in a sample obtained from a test subject;

      (b)   measuring the expression of one or more of a protein

20   shown in Table 2 in a sample obtained from a test subject;
               and

      (c)   comparing the expression of the proteins of steps (a) and
               (b) relative to expression in a control sample;

     wherein changes in a one or more of the proteins of Tables 1 and 2 is

25   indicative of the development of diabetes.

      13.   The method of claim 12, wherein said sample is any one of a cell,

cells, or tissue expressing one or more of the diabetes-mediating proteins listed

in Tables 1 and 2.

      14.   An *in vitro* method of identifying a protective or deleterious

30   diabetes-mediating protein, said method comprising:

      (a)   transfecting a cell with a polynucleotide encoding a
               diabetes-mediating protein under conditions in which the
               polynucleotide is expressed as a protein; and

      (b)   determining the effect of said expressed protein on said

35   cell, wherein said effect is measured as a change in one or
               more cell functions in the absence or presence of a
               cytokine, wherein said cell functions are one or more of
               nitrous oxide (NO) production, insulin secretion, cell
               survival, protein expression, and cytotoxicity.

15.   An *in vivo* method of identifying a protective or deleterious diabetes-mediating protein, said method comprising:

(a)   generating a transgenic mammal expressing a diabetes-mediating protein under conditions in which said protein is expressed; and

(b)   determining the effect of said protein expression on the development and timing of diabetes onset, wherein a protective protein is one which prevents, inhibits, or slows the development of diabetes in a subject at risk for diabetes, and a deleterious protein is one that causes development of diabetes, increases the risk of development of diabetes, increases the severity, or decreases the period of time required for the development of diabetes in a subject at risk for developing diabetes.

16.   A transgenic non-human mammal comprising an exogenous diabetes-mediating protein transgene.

17.   A assay method for screening compounds, wherein said compounds are capable of effecting the expression of a diabetes-mediating protein, comprising:

(a)   administering a test compound to the transgenic mammal of claim 16;

(b)   measuring the effect of said compound on the incidence and timing of the development of diabetes, wherein said compound inhibits, decreases, induces, or increases the expression of said protein.

18.   A compound identified by the assay method of claim 17, characterized as:

(a)   inducing or enhancing the expression of an endogenous protective protein; or

(b)   suppressing or inhibiting the expression of a deleterious diabetes-mediating protein; wherein the compound is capable of delaying or preventing the development of diabetes in a subject at risk for development of diabetes.

19.   A method of treating or preventing diabetes or a diabetes-related disorder, comprising administering a compound capable of preventing or delaying the development of diabetes in a subject at risk for development of diabetes, or capable of ameliorating the symptoms of diabetes in a diabetic subject.

20. The method of claim 19 wherein said compound is an antisense sequence.

21. The method of claim 19 wherein said compound is an antibody specific against a diabetes-mediating protein antibody.

22. The method of claim 19, wherein said compound is a diabetes-mediating protein.

23. The method of claim 22, wherein said diabetes-mediating protein is selected from the group of proteins of Tables 1 and 2.

24. The method of claim 19, wherein said compound enhances or increases the expression of a diabetes-mediating protein.

25. The method of claim 19, wherein said compound inhibits or decreases the expression of a diabetes-mediating protein.

26. The method of claim 25, wherein said compound is a polynucleotide which inhibits the *in vivo* expression of a diabetes-mediating protein.

27. A method for identifying a compound capable of modulating the activity of a diabetes-mediating protein, comprising treating cells, tissues, or animals with a test compound suspected of being capable of modulating the activity of a diabetes-mediating protein, and determining the effect of said compound on the activity of one or more diabetes-mediating protein(s).

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FIG.1A

FIG.1B

MISASRAAAARLVGTAASRSPAAARPQDGWNGLSHEAFRFVSR
DYASEAIKGAVVGIDLGTTNSCVAVMEGKQAKVLENAEGARTTPSVVAFTADGERLV
MPAKRQAVTNPNNTFYATKRLIGRRYDDPEVQKDTKNVPFKIVRASNGDAWVEAHGK
YSPSQIGAFVLMKMKETAENYLGHTAKNAVITVPAYFNDSQRQATKDAGQISGLNVL
VINEPTAAALAYGLDKSEDKVIAVYDLGGGTFDISILEIQKGVFEVKSTNGDTFLGG
DFDQALLRHIVKEFKRETGVDLTKDNMALQRVREAAEKAKCELSSSVQTDINLPYLT
DASGPKHLNMKLTRAQFEGIVTDLIKRTIAPCQKAMQDAEVSKSDIGEVILVGGMTR
PKVQQTVQDLFGRAPSKAVNPDEAVAIGAAIQGGVLAGDVTDVLLLDVTPLSLGIET
GGVFTKLINRNTTIPTKKSQVFSTAADGQTQVEIKVCQGEREMAGDNKLLGQFTLIG
PPAPRGVPQIEVTFDIDANGIVHVSAKDKGTGREQQIVIQSSGGLSKDDIENMVKNA
KYAEEDRRKKERVEAVNMAEGIIHDTETKMEEFKDQLPADECNKLKEEISKVRALLA
KDSETGENIRQAASSLQQASLKLFEMAYKKMASEREGSGSSGTGEQKEDQKEEKQ

FIG.2

MISASRAAAARLVGAAASRGPTAARHQDSWNGLSHEAFRLVSR
DYASEAIKGAVVGIDLGTTNSCVAVMEGKQAKVLENAEGARTTPSVVAFTADGERLV
MPAKRQAVTNPNNTFYATKRLIGRRYDDPEVQKDIKNVPFKIVRASNGDAWVEAHGK
YSPSQIGAFVLMKMKETAENYLGHTAKNAVITVPAYFNDSQRQATKDAGQISGLNVL
VINEPTAAALAYGLDKSEDKVIAVYDLGGGTFDISILEIQKGVFEVKSTNGDTFLGG
DFDQALLRHIVKEFKRETGVDLTKDNMALQRVREAAEKAKCELSSSVQTDINLPYLT
DSSGPKHLNMKLTRAQFEGIVTDLIRRTIAPCQKAMQDAEVSKSDIGEVILVGGMTR
PKVQQTVQDLFGRAPSKAVNPDEAVAIGAAIQGGVLAGDVTDVLLLDVTPLSLGIET
GGVFTKLINRNTTIPTKKSQVFSTAADGQTQVEIKVCQGEREMAGDNKLLGQFTLIG
PPAPRGVPQIEVTFDIDANGIVHVSAKDKGTRREQQIVIQSSGGLSKDDIENMVKNA
KYAEEDRRKKERVEAVNMAEGIIHDTETKMEEFKDQLPADECNKLKEEISKMRELLA
KDSETGENIRQAASSLQQASLKLFEMAYKKMASEREGSGSSGTGEQKEDQKEEKQ

FIG.3

MADGFSLNDALAGSGNPNPRGWPGAWGNQPGAGGYPGASYPGA
PGQAPPGGYPGQAPPSAYPGPTGPSAYPGPTAPGAYPGPTAPGAFPGQPGGPGAYPS
PGAYPSAPGAYPATGPFGAPTGPLTVPYDMPLPGGVMPRMLITIIGTVKPNANSITL
FKKGNDIAFHFNPRFNENNRRVIVCNTKQDNNWGREERQSAFPPFESGKPFKIQVLVE
DHFKVAVNDVHLLQYNHRMKNLREISQLGIIGDITLTSASHAMI

FIG.4

MADNFSLHDALSGSGNPNPQGWPGAWGNQPAGAGGYPGASYPG
YPGQAPPGAYPGQAPPGAYHGAPGAYPGAPAPGVYPGPPSGPGAYPSSGQPSAPGAY
ATGPYGAPAGPLIVPYNLPLPGGVVPRMLITILGTVKPNANRIALDFQRGNDVAFHF
PRFNENNRRVIVCNTKLDNNWGREERQSVFPFESGKPFKIQVLVEPDHFKVAVNDAH
LQYNHRVKKLNEISKLGISGDIDLTSASYTMI
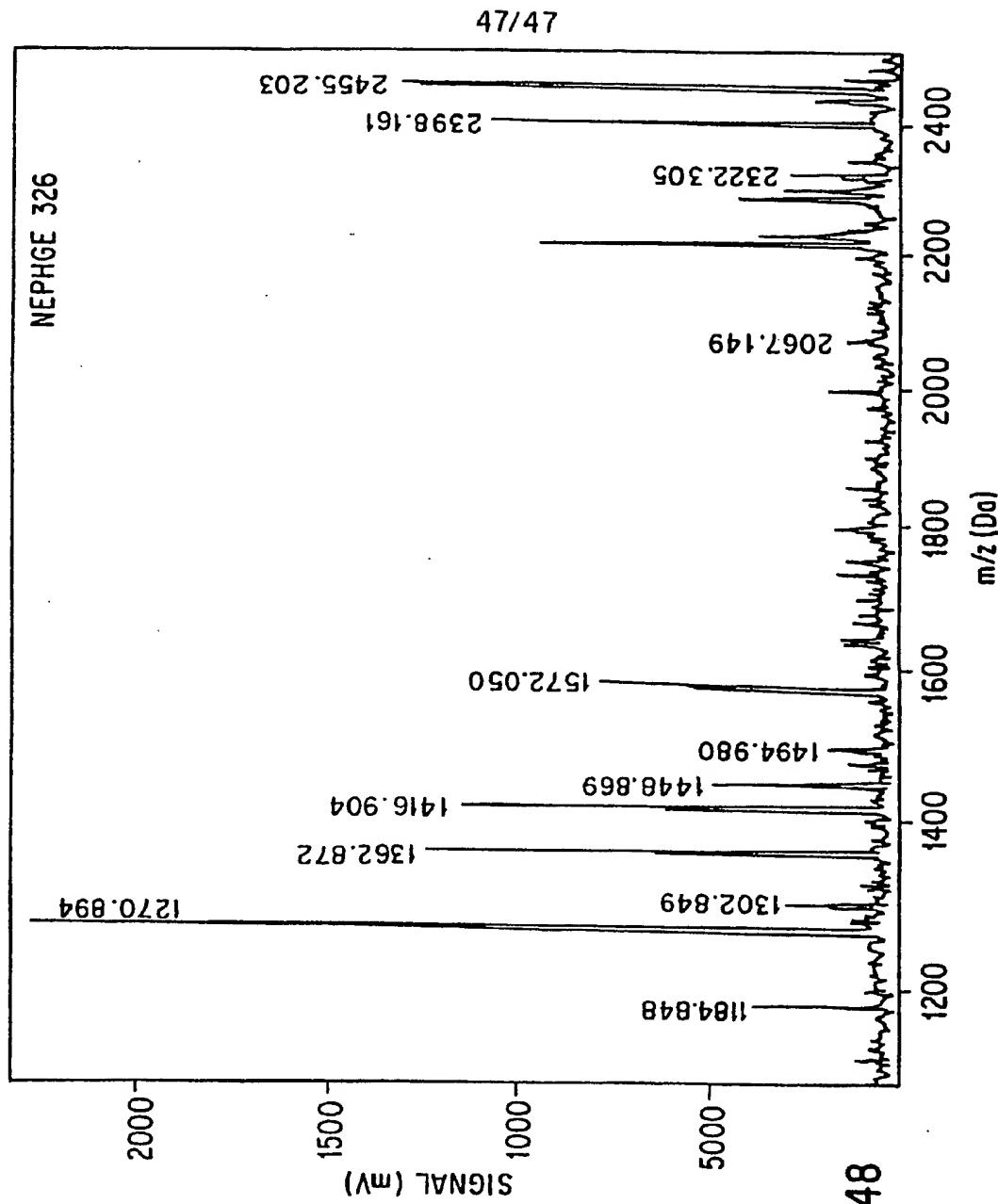
FIG.5

SUBSTITUTE SHEET (RULE 26)

FIG.6

FIG.7

FIG.8

FIG.9

FIG.10

FIG.11

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FIG.12

FIG.13

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FIG.14

FIG.15

FIG.16

FIG.17

FIG.18

FIG.19

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FIG.20

FIG. 21

FIG.22

FIG.23

FIG.24

FIG. 25

FIG.26

FIG.27

FIG.28

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FIG.34

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FIG.35

FIG.36

FIG. 37

FIG.38

FIG.39

FIG. 40

Fig. 41

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FIG. 43

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FIG.44

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FIG.45

Fig. 46

FIG.47

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FIG. 48